

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
12 September 2003 (12.09.2003)

PCT

(10) International Publication Number
WO 03/074553 A2

(51) International Patent Classification⁷: C07K 14/245

(21) International Application Number: PCT/EP03/02925

(22) International Filing Date: 6 March 2003 (06.03.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
02290556.6 6 March 2002 (06.03.2002) EP

(71) Applicant (*for all designated States except US*): MUTA-
BILIS SA [FR/FR]; 13, rue de Toul, F-75012 Paris (FR).

(72) Inventor; and

(75) Inventor/Applicant (*for US only*): ESCAICH, Sonia
[FR/FR]; 13, rue de Toul, F-75012 Paris (FR).

(74) Agents: PEAUCELLE, Chantal et al.; Cabinet Armen-
gaud Aine, 3, Avenue Bugeaud, F-75116 Paris (FR).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NEW PRODUCTS SPECIFIC TO PATHOGENIC STRAINS AND THEIR USE AS VACCINES AND IN IMMUNOTHERAPY

(57) Abstract: The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of: 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria, 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates, 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates, 4- testing the polypeptides for immunogenicity using animals models. Application for making vaccines compositions and immunotherapies

BEST AVAILABLE COPY

New products specific to pathogenic strains and their use as
vaccines and in immunotherapy

The invention relates to new products specific to pathogenic
5 strains, particularly to extra-intestinal *E. coli* strains.

It more particularly relates as products to antigenic
polypeptides and antibodies directed against said polypeptides
and to their use as vaccines and in immunotherapy,
10 respectively.

Although *Escherichia coli* is probably the best known bacterial
species and is one of the most common isolated in clinical
microbiology laboratories, misconceptions abound regarding the
15 various types of *E. coli* and the infections they cause.

E. coli strains of biological significance to humans can be
broadly classified in 3 major groups:

1. Commensal strains, which are part of the normal flora.
- 20 2. Intestinal pathogenic strains, which are not part of
the normal flora. This group contains various pathotypes
(EPEC, EHEC, ETEC, EIEC) not including *Shigella*.
3. Extra-intestinal strains (ExPEC) which are responsible
for infections outside the gastro-intestinal (GI) tract, but
25 can also be part of the normal flora. All hosts, either
immunocompromised or not are susceptible to these infections.

ExPEC strains are responsible for the majority of the urinary
tract infections (UTI) particularly cystitis, pyelonephritis,
30 and catheter associated infections.

They are also responsible for abdominal infections, nosocomial
pneumoniae, neonatal meningitis, soft tissue infections, and
bone infections. Each one of these localizations can lead to

bacteremia with a risk of sepsis in case of organ failure. ExPEC strains are indeed the most common Gram negative bacilli isolated from blood cultures.

5 750 000 cases of bacterial sepsis occur each year in the US, and are responsible for 225 000 deaths. In a recent study on 1690 cases of sepsis, it was shown that the main bacteria species identified is ExPEC (16% of the cases) and then *S.aureus* (14% of the cases).

10.

These numbers demonstrate the importance of ExPEC strains in both hospital and community acquired infections.

15 ExPEC strains correspond to a homogenous subset of *E. coli* strains. Analysis of phylogenetic relationships among *E. coli* strains by MLEE has revealed that *E. coli* belong to 4 main phylogenetic groups designated A, B1, B2 and D.

20 The pathogenesis of ExPEC strains is that of extra-cellular microorganisms, i.e., they are well adapted to growth in the extra-cellular fluids and efficiently resist phagocytosis by polymorphonuclear. Initial studies have shown that virulence factors known to be important for the extra-cellular growth are mainly found in B2/D *E. coli*., thus suggesting that B2/D
25 subgroups contain most of the ExPEC strains. This was reinforced by experiments performed on animals showing that B2/D strains are more virulent than A and B1 strains. Subsequent epidemiological studies have indeed confirmed these hypotheses. B2/D isolates are those predominantly responsible
30 for neonatal meningitidis (87%) and community or nosocomial acquired urosepsis, (93 % and 85%, respectively).

Similar results have been reported for cystitis (70% are due to the sole B2 *E. coli*), thus demonstrating that the importance of ExPEC strains.

- 5 These recent findings demonstrate that the B2/D subgroup of strains is the *E. coli* core genome the best adapted to growth in extra-cellular fluids.

10 In addition to this core genome, ExPEC strains have various pathogenicity islands which encode virulence factors associated with the different pathogenesis of extra-intestinal *E. coli* infections (UTI, urosepsis, neonatal meningitidis...). Among the main virulence factors are the capsule, which is well-known to be important for extra-cellular growth, and the
15 iron chelation systems (aerobactin and enterochelin, for example). In addition, depending on the pathogenesis, these strains can produce toxins (CNF, hemolysin...), adhesins (pap, sfa...) and other iron chelation systems.

- 20 The notion that B2/D *E. coli* correspond to a distinct subset of pathogenic *E. coli* strains is reinforced by the fact that B2/D *E. coli* are not broadly isolated from the stools of humans. They were recovered from only 11% of individuals, whereas A and B1 subgroups are present in the stools of 74% of
25 the individuals of a human population.

As mentioned above the pathogenesis of ExPEC strains relies on their ability to multiply in the extra-cellular fluids and to resist bactericidal activity of the complement and
30 phagocytosis by polymorphonuclear. Therefore, as for other extra-cellular pathogens (*Haemophilus influenzae*, *Streptococcus pneumoniae* and *Neisseria meningitidis*) a protective antigen against ExPEC has to induce antibodies

that promote opsonisation and/or the bactericidal activity of serum.

5 Considering the above statements, an efficient antigen has to be largely represented among the population of B2/D *E. coli*. Similarly to other extra-cellular pathogens, the capsular polysaccharide would be an ideal antigen, however most pathogenic B2 strains express the K1 polysaccharide. The latter has a structure identical to that of group B
10 meningococcus, which is non-immunogenic and shares common antigens with the brain. Another possible target may be the lipopolysaccharide (LPS). However there are a large number of different LPS serotypes that are shared by various subgroups.

15 The inventors have now found that some specific components coded by the B2/D genome, but absent from A and B1 *E. coli* strains, are particularly useful as antigens and can specifically prevent the pathologies due to ExPEC strains. Homologs of these antigenic components can be found in other
20 pathogenic bacterial species and therefore are useful to prevent the pathologies caused by these bacteria. Accordingly, any reference to products specific to ExPEC strains and to their uses will encompass components in these species.

25 For example homologous antigens could be present in the following species and be as such used for prevention of disease due to the bacteria:

30 *Pseudomonas aeruginosa*, *Escherichia coli* O157:H7, *Yersinia pestis*, *Vibrio cholerae*, *Legionella pneumophila*, *Salmonella enterica*, *Salmonella typhimurium*, *Haemophilus influenzae*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,

Clostridium botulinum, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Pseudomonas aeruginosa*,
5 *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*,
10 and any species falling within the genera of any of the above species.

It is then an object of the invention to provide new isolated antigenic polypeptides, and polynucleotides belonging to the core B2/D genome and not present in commensal *E. coli*.

15 Another object of the invention is to provide antibodies raised against such antigenic polypeptides, or peptidic fragments.

20 It is still another object of the invention to provide vectors and host cells containing said polynucleotides.

Another object of the invention is to provide vaccine compositions specific to extra intestinal infections caused by
25 ExPEC and pathologies caused by other pathogenic strains expressing antigenic polypeptides homologous to the ExPEC antigenic polypeptides.

The invention also relates to means for detecting and treating
30 a development of *E. coli* in a human or animal compartment which is extra-intestinal (systemic and non-diarrhoeal infections, such as septicaemia, pyelonephritis, or meningitis in the newborn).

The isolated antigenic polypeptides used according to the invention are selected among polypeptides specific to B2/D *E. coli* strains and not present in A and B1 isolates of *E. coli*. They are encoded by genes belonging to the core B2/D genome and are not present in commensal *E. coli*.

They have a sequence selected in the group comprising the sequences of SEQ ID N°11 to N°66 or 133-145 or homologous sequences with a minimum of 25% of identity with the whole sequences SEQ ID N°11 to N°66, or 133-145, respectively.

The isolated polypeptides having SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138 are new polypeptides and therefore are part of the invention.

The invention also relates to homologous isolated antigenic peptides, comprising polypeptides having at least 25% identity to a polypeptide having a sequence SEQ ID N° as above defined, more particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide having a sequence corresponding to said SEQ ID N°s, as determined using BLASTP or BLASTX with the default parameters.

Said polypeptides are obtainable by a process comprising the steps of :

- a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria,

- b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- c- purifying the polypeptides identified in step a, which are found in step 2 to be conserved in the B2/D isolates,
- 5 d- testing the polypeptides for immunogenicity using animals models.

By the term "conserved", it is meant, according to the invention, that the genes coding for the polypeptides are
10 present with a frequency of at least 50% in B2/D isolates, preferably greater than 60%, more preferably greater than 80% and even more preferably greater than 85%, and in less than 40% in A/B isolates; preferably in less than 20%, more preferably in less than 15%.

15 The animal models used in step c are infected adult animals, eventually immunodepressed.

The adult animals particularly mice, are infected
20 intraperitoneally, the endpoint being the animal death and/or bacteremia measurement.

The animals can be immunodepressed by injection, for example, of cyclophosphamide which induces a neutropenia. Such a model
25 will validate the use of the antigen for prevention of *E. coli* sepsis in immunodepressed patients. Another animal model could be for example 2 to 3 day old infant mice.

The variants or fractionnal sequences conserving the B2/D
30 properties and which are antigenic as defined in step 4 of the above process are also part of the invention. The term "variant" is herein intended to mean any sequence having insertions and/or deletions and/or substitutions with respect

to the parent sequence. The term "fractional" is herein intended to mean any fragment of the parent sequence.

The invention also relates to the use of isolated polynucleotides coding for a polypeptide such as above defined according to the universal genetic code and taking into account the degeneracy of this code. The term "polynucleotide" encompasses any nucleotidic sequence such as DNA, including cDNA, RNA, including mRNA.

Said polynucleotides have preferably sequences corresponding to SEQ ID N°77 to SEQ ID N°132 or 146 to 158 .

More preferably, said polynucleotides have sequences corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

The invention also relates to the homologs to said polynucleotides . Said homologs may have at least 25% identity to a polynucleotide having said sequences, or at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a polynucleotide having one of said SEQ ID N°s, as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.

The present application is also aimed towards any vector comprising at least one of said polynucleotides and also any cell transformed by genetic engineering, characterized in that it comprises, by transfection, at least one of said

polynucleotides and/or at least one vector according to the invention, and/or in that said transformation induces the production by this cell of at least one polypeptide corresponding to a polynucleotide such as above-defined.

5

The invention also relates to a process for isolating and identifying antigenic polypeptides, therefore useful as vaccine for *E. coli*.

10 Such a process comprises the steps of

- a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
- 15 b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- c- purifying the polypeptides identified in step a, which are found in step 2 to be conserved in B2/D isolates,
- d- testing the polypeptides for immunogenicity using animals
- 20 models.

The selected antigenic polypeptides, alone or in combination, are capable of inducing an antibody response for prevention of infections due to ExPEC strains regardless of the pathogenesis

25 and of the infection site (UTI, pyelonephritis, sepsis, bacteremia, neonatal meningitis).

Such polypeptides particularly have sequences SEQ ID N°1 to SEQ ID N°66, or 133-145 or correspond to homologous sequences.

30

The invention thus relates to vaccine compositions specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide or fragment thereof as above defined, with a carrier, particularly at

least one polypeptide of SEQ ID N°1 to SEQ ID N°66, except SEQ ID N°8, and 133-145 and the homologous polypeptides.

Such vaccine compositions are particularly useful for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.

The vaccine compositions of the invention are indicated for :

- immunodepressed patients, ideally before the start of the immunosuppressive therapy : patients suffering from cancer, diabetes, leukaemia, transplant patients, patients receiving long-term steroids therapy.
- Patients before surgery where there is a high risk of *E. coli* infections (abdominal surgery).
- In all these cases, the *E. coli* vaccine of the invention could be administered in association with a *Staphylococcus aureus* vaccine,
- Patients with recurrent UTI, especially after one episode of pyelonephritis.
- The prevention of neonatal infections will require vaccination of the mother, implying vaccination long before pregnancy to avoid potential problem. Ideally such a vaccine should be associated with a Group B *Streptococcus* polysaccharide vaccine in order to also prevent late onset neonatal infections. It should be pointed out that the induction of a level of antibodies against B2/D *E. coli* in pregnant women would also prevent UTI, which are always a risk in the context of a pregnancy.

The formulation and the dose of said vaccine compositions can be developed and adjusted by those skilled in the art as a function of the indication targeted, of the method of

administration desired, and of the patient under consideration (age, weight).

5 These compositions comprise one or more physiologically inert vehicles, and in particular any excipient suitable for the formulation and/or for the method of administration desired.

10 For example the vaccine could be a suspension of the purified polypeptide in sterile water with aluminium based mineral salt as adjuvant and be administered subcutaneously with a first and boosting injection.

15 The antibodies raised against the above-identified polypeptides are also part of the invention.

20 They are capable of binding to said polypeptides in physiological-type conditions (in vivo or mimicking in vivo) when administered to a human or animal organism, and ELISA-type conditions when said binding product is intended to be used in assays and methods in vitro. Such antibodies advantageously inhibit the extra-intestinal growth of ExPEX strains in human or animal.

25 They are particularly useful for immunotherapy applications with antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody (Mab) will be derived from the peptides or
30 polypeptides.

The methods for manufacturing such antibodies using the polypeptides according to the invention are available to those skilled in the art. They are conventional methods which

comprise, in particular, the immunization of animals such as rabbits and the harvesting of the serum produced, followed optionally by the purification of the serum obtained. A technique suitable for the production of monoclonal antibodies is that of Köhler and Milstein (Nature 1975, 256:495-497).

Said antibodies do not recognize the cells of the human or animal to which it is intended.

In particular for immunotherapy applications with monoclonal antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody will be derived from the peptides or polypeptides.

The antibodies or fragments thereof are advantageously humanized when intended for a human administration.

Alternatively, humanized Mab could be derived from murine or rat Mab specific of the antigen. These fully humanized Mab are constructed using conventional molecular techniques to graft complementarity-determining regions from the parent murine or rat antibacterial antibody into human IgG1 kappa heavy and light-chain frameworks.

The present invention is also aimed towards the use, in an effective amount, of at least one of polypeptides having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, antibodies or polynucleotides for the diagnosis of the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection.

The detection of the presence or absence of such compounds can in particular be carried out by nucleotide hybridization, by PCR amplification or by detection of their polypeptide products. Detection of the presence of such compounds makes it possible to conclude that a B2/D *E. coli* strain is present.

The invention also relates to pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide as above defined, particularly having SEQ ID N°1-66 to 133-145, in combination with a pharmaceutically acceptable carrier.

Preferred pharmaceutical compositions comprise at least one polypeptide having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138,

The present application is also aimed towards any use of a polypeptide such as above defined for the manufacture of a composition, in particular of a pharmaceutical composition, intended to alleviate and/or to prevent and/or to treat an undesirable growth of *E. coli*, such as an *E. coli* infection, (for example systemic and non-diarrhoeal infections), the presence of extra-intestinal *E. coli* or a sanitary contamination.

The present invention is illustrated by the examples which follow and which are given in a non limiting capacity and with reference to figures 1 and 2, wherein

- Figure 1 represents a protein purification result after cloning and expression, and

- Figure 2 is a picture of the DNA array after hybridization with the genomic DNA from a B2/D reference strain.

5 Example 1: Assay for the immunogenicity of a selected polypeptide from sequences 1-66 and 133-145 (except SEQ ID N°8)

10 . Cloning expression and purification of the selected polypeptide.

The nucleic acid having SEQ ID N°95 encoding the polypeptide corresponding to SEQ ID N°28 was cloned without the signal sequence (coding the 16 first amino acids) in a prokaryotic expression vector according to classical methods for cloning. 15 The recombinant plasmid was used to transform the *E. coli* strain BL21. Transformed cells containing the recombinant plasmid were selected in LB medium with 100µg/ml ampicillin. Individual clones are picked and grown in presence of IPTG 1mM 20 to induce recombinant protein expression. Total protein content of the culture cells was extracted by cell lysis. Recombinant protein was purified by affinity columns.

25 Protein purification after cloning and expression

Total cell lysat of IPTG-induced bacteria were mixed with Ni-NTA matrix (Qiagen®) for 60 min et 4°C and loaded into a column. After washing the column to remove non specific binding, the recombinant protein was eluate 3 times with 1 ml 30 elution buffer pH 5.9. The protein was then eluate 4 times with 1 ml elution buffer pH 4.5.

Figure 1 represents a Coomassie blue stained SDS gel of recombinant protein after affinity column purification: PM:

markers E1-4: sample collected from each purification fraction. Arrow indicate the band corresponding to the recombinant protein.

5 . Test for immunogenicity in an animal model

Polypeptide preparation from SEQ ID N°28 was injected to Swiss mice to induce an antibody response as follows :

10 At d0 a first immunisation was done by injecting 20 μ g of the protein at in 100 μ g solution of PBS and complet Freund adjuvant (1:1). Control animals were injected with 100 μ l solution of PBS and complet Freund adjuvant (1:1).

15 Boosting injection at d21 with 10 μ g of protein in 100 μ l PBS and complet Freund adjuvant (1:1).

Sera from vaccinated animals was prepared from blood drawn by puncture in the tail of the mice.

20

Detection of specific antibodies in animal sera, at d20 before the boosting injection, was performed by western blot according to standart protocol. Purified polypeptide was subjected to electrophoresis (10 μ g per lane) and transfert to
25 nitrocellulose membrane.

The membranes were then saturated by incubation 35 min with PBS/Tween20 0.1%/powder milk 5%.

30 Diluted sera was incubated with the membrane for 45 min. Membranes were washed three time 5 min with PBS/tween. Bound antibodies were then recognized by an anti-mouse IgG coupled to horseradish peroxidase enzyme. After washing 3 times with PBS/Tween and 3 time with PBS, enzymatic activity was revealed

by addition of chromogenic substrate DAB and hydrogen peroxyde.

5 Results : Sera from vaccinated animal, diluted at 1/100 revealed a unique band corresponding to the injected polypeptide. No antibody to the polypeptide could be detected in sera from control animals.

10 At d42, 300 μ l of cyclophosphamide and 200 μ l at d45 were injected IP in the mice to induce neutropenia in order to increase the susceptibility to the challenge infection.

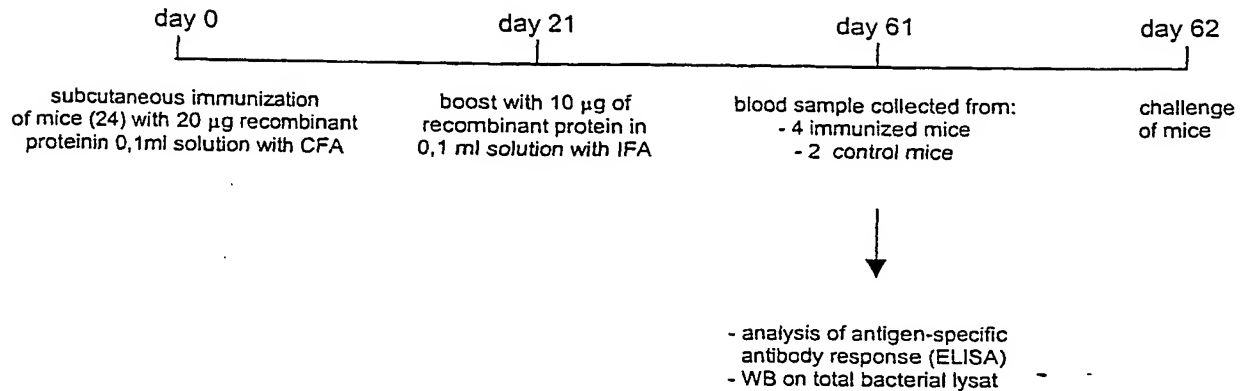
At d46 vaccinated and control mice were challenged by intraperitoneal injection of the wt B2/D strain C5 of *E. coli* at a dose equal to 10 time the LD50 (letal dose).

15 Immunogenicity of the selected polypeptide and protection conferred by vaccination with the seleted polypeptide was assessed by the survival of vaccinated animals three days post challenge.

20 Another example of vaccination to demonstrate immunogenicity of polypeptides:

- 24 Balb/c mice, female, 6 weeks old were immunized by
25 subcutaneous Injection of the protein in Complete Freund's adjuvant, and 14 control mice were injected with CFA and PBS
- 3 weeks later a boost injection of 10 μ g of protein in with incomplete Freund's adjuvant.

VACCINATION PROTOCOL



15 Before challenge at d62, sera was collected at d61 to analyze the antibody response in the vaccinated animals.

- WB analysis of sera from immunized mice were performed to detect the antibody response to the recombinant proteins used for immunization as described above.

- An ELISA assay was set up to measure antibody titer in vaccinated animals:

- Each recombinant protein was coated on a 96-well plates with (200 ng/100 µl coating buffer), plates are saturated with 3%BSA in PBS.
- Twofold serial dilution of sera were made in PBS 1X/1% BSA from 1:500, to 1: 1024000 and incubated on the plate, antibody binding was revealed using a rabbit Anti-mouse IgG conjugated with Peroxydase and OPD(o-phenylenediamine) chromogen substrate.
- Read the OD₄₉₅ with Sanofi Diagnostics Pasteur PR2100®

- Results:

Table 1. Sera titer against recombinant protein by ELISA

SEQ ID	serum1	serum 2	serum 3	serum 4	Control	recombinant protein
2	128	64	128	512	<0,5	
140	>64	>64	>64	>64	<0,5	+
31	>64	>64	>64	>64	<0,5	+
49	>64	>64	>64	>64	<0,5	+
51	>64	>64	>64	>64	<0,5	+
25	>64	>64	>64	>64	<0,5	+
7	16	8	>64	<0,5	<0,5	+
19	>64	>64	>64	>64	0,5	+
3	>64	>64	>64	>64	<0,5	+
26	512	128	64	256	<0,5	+
18	>64	>64	>64	>64	0,5	+
32	>64	>64	>64	>64	0,5	+
53	>64	>64	>64	>64	0,5	+
587	>64	16	32	32	<0,5	+
11	>64	32	32	64	<0,5	+
36	512	256	512	256	<0,5	+
10	32	128	256	128	0,5	+
47	512	512	512	512	0,5	+
20	1024	256	256	512	<0,5	+
17	1024	512	128	512	<0,5	+

5

- To assess the ability of sera to recognize the native antigen expressed by the bacteria, western blot was also performed on whole bacteria lysat.

10 To this end, bacteria were grown in LB medium supplemented or not with iron chelator until OD600=0.5-0.6 and pelleted by centrifugation 5 minutes at 10000 rpm. The pellet was lysed by resuspension in 1X loading buffer containing SDS and heated 5 min at 95°C before migration on the gel. Western blot assay was

15 then performed with sera from controls and vaccinated animals.

Results in table 2 shows the results obtained with Sera from vaccinated mice against recombinant protein and against *E.coli* lysat.

- 5 Table 2: reactivity in Western Blot of sera from mice vaccinated with polypeptides encoded by the different ORFs

SEQ ID N°	whole cell lysate	recombinant protein
2	+	+
140	+	+
26	+	+

- 10 • Protection assay, end point: mortality

At d62, 20 vaccinated and 10 control mice were challenged with an *E.coli* virulent strain belonging to B2 group at a dose equal to the LD 50 (5.10^5 cfu/mice) by intraperitoneal
 15 injection. Mortality is recorded at 48h, results in Table 3 are expressed as a percentage of protection representing the difference of survival in vaccinated versus control mice groups.

- 20 Table 3 : Protection obtained in mice challenged after immunization with proteines encoded by the corresponding ORFs.

SEQ ID N°	% protection
2	52
26	66
36	46
10	30
47	60
20	25

- 25 • Protection assay, end point: bacteremia

30 At d62, 10 vaccinated and 5 control mice were challenged with an *E.coli* virulent strain belonging to B2 group at a dose equal to the 1/5 of the LD 50 (1.10^5 cfu/mice) by intraperitoneal

injection. With this infectious dose the mice survived the infection at d48. At 48h blood was collected for each mice in presence of heparin. To assess bacteremia, the blood was plated on LB media and colonies count measured after overnight culture.

Example 2: Distribution of the DNA sequence of ORFs specific for B2/D group of *E.coli* in clinical isolates.

10 To make a DNA arrays membrane specific for B2/D group of *E.coli*, DNA corresponding to ORFs that were identified as specific for B2/D core genome of *E.coli* was amplified by PCR and spotted on nylon membrane using standard methods to those skilled in the art.

15 Chromosomal DNA from 30 *E.coli* clinical isolate strains (of which 23 were from pathological conditions and 6 isolated from human normal flora), was prepared and radiolabelled with ³²P.

20 DNA from these clinical isolates was then hybridized to the B2/D specific DNA array, the results were read by a phosphoimager and spots reactivity was analyzed with an image analysis software. If hybridization gave a positive signal
25 for a particular ORF, this ORF is considered to be present in the genome of the isolate. Quality control of the array is the hybridization of a probe DNA from a reference strain of *E.coli* as shown in figure 2, which represents a picture of the DNA array after hybridization with the genomic DNA from a B2/D
30 reference strain.

The details of the method used for these experiments has been described previously in Tinsley et al. *Methods Enzymol.* 2002, 358; 188-207.

- 5 Results presented in Table 4 are expressed as the frequency of each ORF detection in the three different group A, B and D of *E.coli* strains.
- 10 Table 4 : Presence of Orfs encoding antigens in *E.coli* clinical isolate genomes

Frequency of positive signal %	Clinical isolate groups		
	A	D	B2
SEQ ID N°	N=6	n=5	n=18
86	17	20	100
119	0	80	100
137	0	0	100
77	0	100	94
78	0	100	100
79	0	100	100
80	0	0	100
84	0	0	100
82	0	0	100
88	0	0	100
83	0	0	94
85	0	0	78
88	0	0	56
81	33	20	100
89	33	60	67
90	0	0	61
91	17	80	67
94	0	0	100
92	0	0	100
93	0	0	100

96	0	100	100
85	17	100	100
97	0	70	100
98	0	0	100
99	0	0	78
101	0	80	100
102	0	0	100
104	0	0	11
103	0	0	100
105	0	0	67
100	0	100	100
111	17	0	61
115	0	0	78
114	0	0	83
113	0	0	94
120	33	80	16
125	17	0	89
109	0	0	33
110	0	0	17
124	0	0	72
126	0	80	78
116	0	0	33
112	0	0	22
106	17	0	33
117	33	80	11
132	33	80	22
122	0	0	22
74	0	0	89
70	0	0	33
73	0	0	89
71	50	100	22
75	0	0	0
76	0	0	56
67	0	0	50

69	100	100	100
68	67	100	100
152	0	0	94
153	0	100	100
150	0	0	11
142	83	100	78
157	67	0	94
156	17	100	100
100	0	100	100
154	0	80	67
147	0	0	100
146	17	100	100
158	17	100	89
107	17	0	78
72	50	100	44
151	0	0	11
149	0	0	28
148	0	0	6

Example 3 : Vaccines compositions intended for prevention of any form of infection by ExPEC.

- 5 The polypeptide coded by a sequence comprising SEQ ID N°28 is conjugated with a toxin and added to a physiologically inert vehicle.

10 This conjugated peptide is optionnally added to a childhood vaccine.

The composition is sterilized and can be injected parenterally, subcutaneously or intramuscularly.

- 15 Said composition can also be sprayed onto mucosa with the aid of a spray.

CLAIMS

1.The isolated polypeptides having SEQ ID N° 14, 15, 17, 21,
22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to
5 55, 58, 60, 63, 133-138.

2- Isolated antigenic polypeptides according to claim 1
obtainable by a process comprising the steps of :

- 10 a- selecting on the basis of sequence analysis those of the
polypeptides which are either located in the outer membrane or
secreted by the bacteria,
b- identifying the genes coding for said polypeptides which
are conserved in B2/D clinical isolates,
c- purifying the polypeptides identified in step a, which are
15 found in step b to be conserved in B2/D isolates,
d- testing the polypeptides for immunogenicity using animals
models.

3. Isolated polynucleotides, coding for a polypeptide
20 according to claim 1 or 2, according to the universal genetic
code.

4. Isolated polynucleotides according to claim 3, having
sequences selected in the group comprising SEQ ID N° 80, 81,
25 83, 87-89, 94-96, 98, 102, 104, 105, 107-110, 112, 115, 116,
118, 119, 126, 127, 130, 132, 135, 146-151.

5. An expression vector comprising at least an isolated
polynucleotide according to claim 3 or 4.

30

6. A host cell comprising an expression vector according
to claim 5.

7. A process for isolating and identifying antigenic polypeptides, useful as vaccines comprising the steps of :

- a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or
5 secreted by the bacteria,
- b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
- c- purifying the polypeptides identified in step a, which are found in step b to be conserved in B2/D isolates,
- 10 d- testing the polypeptides for immunogenicity using animals models.

8. The process of claim 7, comprising the use of infected adult animals, eventually immunodepressed, and of infant
15 animals as models for neonatal infections.

9. The use of at least one polypeptide or fragment of these polypeptides selected in the group comprising SEQ ID N°1 to SEQ ID N°66 (except SEQ ID N°8), or 133-145 as antigens and
20 the homologous sequences.

10. A vaccine composition specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide such as selected by the
25 process of claim 7, or according to claim 9, alone or in combination, particularly at least one polypeptide having a sequence selected in the group comprising SEQ ID N°1 to SEQ ID N°66, or 133-145, except SEQ ID N°8 and the homologous sequences, with a carrier.

30

11. The vaccine composition of claim 10 for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitidis.

12. The vaccine composition of claim 10 or 11, adapted to specific indication in combination with components directed against other bacteria, such as *S.aureus* or group B *Streptococcus*. Or other bacteria implicated in systemic
5 infections.

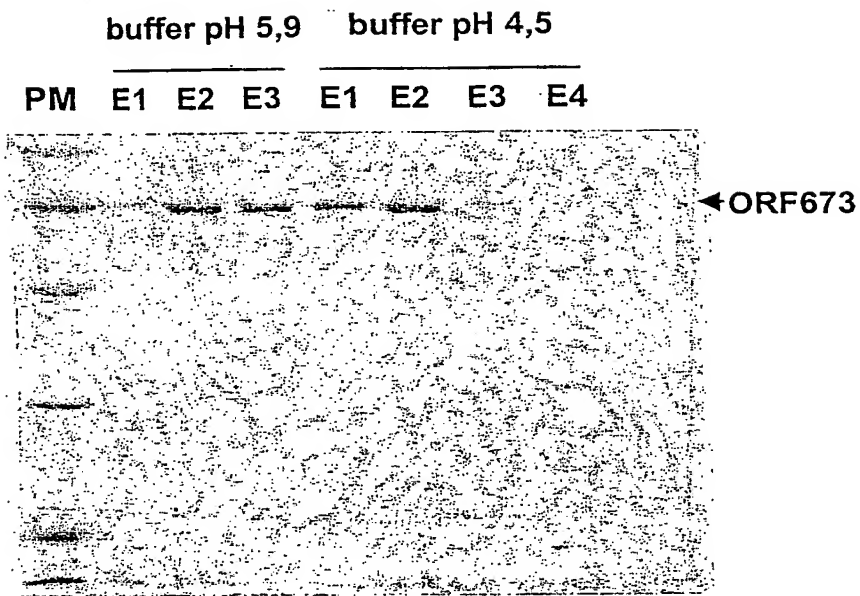
13. Antibodies or fragments thereof directed against a polypeptide such as used according to claim 9.

10 14. Monoclonal antibodies against epitopes of polypeptide and there use as pharmaceutical compound for treatment or prevention of severe infection due to Expec in neonates and patients at risk for such infections.

15 15. A method for detecting the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection, comprising the use of at least one polypeptide such as defined in claim 1 or 2 or a polynucleotide according to claim 3 or 4, or an antibody to
20 claim 13 or 14, said polypeptide(s) being optionally in combination with anyone of the polypeptides having SEQ ID N°1-66 to 133-145.

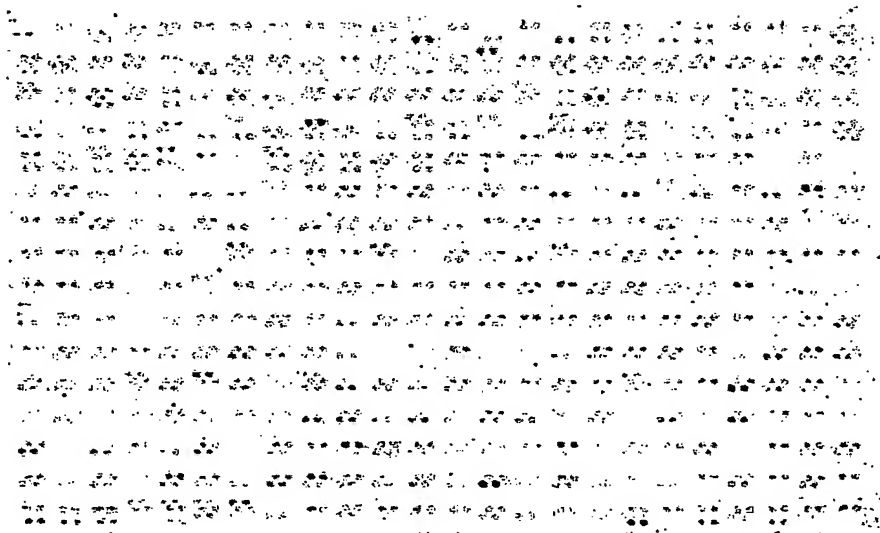
25 16. Pharmaceutical composition for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide according to claim 9, in combination with a pharmaceutically acceptable carrier.

1/2

FIGURE 1

2/2

FIGURE 2



SUBSTITUTE SHEET (RULE 26)

SEQUENCE LISTING

<110> MUTABILIS
 <120> New products specific to pathogenic strains and their
 use as vaccines and in immunotherapy
 <130> 1494
 <160> 132
 <170> PatentIn version 3.1
 <210> 1
 <211> 163
 <212> PRT
 <213> Escherichia coli
 <400> 1

Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile
 1 5 10 15

Val Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Asn
 20 25 30

Val Leu Gln Arg Thr Cys Asn Val Pro Gly Asn Val Asp Val Ser Leu
 35 40 45

Gly Asn Leu Tyr Val Ser Asp Phe Pro Asn Ala Gly Ser Gly Ser Pro
 50 55 60

Trp Val Asn Phe Asp Leu Ser Leu Thr Gly Cys Gln Asn Met Asn Thr
 65 70 75 80

Val Arg Ala Thr Phe Ser Gly Thr Ala Asp Gly Gln Thr Tyr Tyr Ala
 85 90 95

Asn Thr Gly Asn Ala Gly Gly Ile Lys Ile Glu Ile Gln Asp Arg Asp
 100 105 110

Gly Ser Asn Ala Ser Tyr His Asn Gly Met Phe Lys Thr Leu Asn Val
 115 120 125

Gln Asn Asn Asn Ala Thr Phe Asn Leu Lys Ala Arg Ala Val Ser Lys
 130 135 140

Gly Gln Val Thr Pro Gly Asn Ile Ser Ser Val Ile Thr Val Thr Tyr
 145 150 155 160

Thr Tyr Ala

<210> 2
 <211> 673
 <212> PRT
 <213> Escherichia coli
 <400> 2

Met Lys Met Thr Arg Leu Tyr Pro Leu Ala Leu Gly Gly Leu Leu Leu
 1 5 10 15

Pro Ala Ile Ala Asn Ala Gln Thr Ser Gln Gln Asp Glu Ser Thr Leu
 20 25 30

Val Val Thr Ala Ser Lys Gln Ser Ser Arg Ser Ala Ser Ala Asn Asn
 35 40 45

Val Ser Ser Thr Val Val Ser Ala Pro Glu Leu Ser Asp Ala Gly Val
 50 55 60

Thr Ala Ser Asp Lys Leu Pro Arg Val Leu Pro Gly Leu Asn Ile Glu
 65 70 75 80

Asn Ser Gly Asn Met Leu Phe Ser Thr Ile Ser Leu Arg Gly Val Ser
 85 90 95

Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly
 100 105 110

Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln
 115 120 125

Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser
 130 135 140

Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr
 145 150 155 160

Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg
 165 170 175

Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly
 180 185 190

Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro
 195 200 205

Ala Thr Gly Ser Asp Asp Leu Gly Gly Thr Arg Ala Ser Ile Gly Asn
 210 215 220

Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe
 225 230 235 240

Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly
 245 250 255

Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro
 260 265 270

Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys
 275 280 285

Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln
 290 295 300

Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met
 305 310 315 320

Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu
 325 330 335

Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn
 340 345 350

Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr
 355 360 365

Leu Ser Ser Thr Gly Tyr Thr Thr Ala Glu Thr Leu Ala Ala Tyr Ser
 370 375 380

Asp Leu Thr Trp His Leu Thr Asp Arg Phe Asp Ile Gly Gly Gly Val
 385 390 395 400

Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu
 405 410 415

Gly Asn Pro Phe Gly Asp Gln Gly Lys Ser Asn Asp Asp Gln Val Leu
 420 425 430

Gly Gln Leu Ser Ala Gly Tyr Met Leu Thr Asp Asp Trp Arg Val Tyr
 435 440 445

Thr Arg Val Ala Gln Gly Tyr Lys Pro Ser Gly Tyr Asn Ile Val Pro
 450 455 460

Thr Ala Gly Leu Asp Ala Lys Pro Phe Val Ala Glu Lys Ser Ile Asn
 465 470 475 480

Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala
 485 490 495

Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro
 500 505 510

Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly
 515 520 525

Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp
 530 535 540

Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu
 545 550 555 560

Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser
 565 570 575

Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg
 580 585 590

Leu Ala Val Asn Leu Val Gly Pro His Tyr Phe Asp Gly Asp Asn Gln
 595 600 605

Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln
 610 615 620

Ala Thr Glu Arg Met Asn Ile Ser Val Tyr Val Asp Asn Leu Phe Asp
 625 630 635 640

Arg Arg Tyr Arg Thr Tyr Gly Tyr Met Asn Gly Ser Ser Ala Val Ala
 645 650 655

Gln Val Asn Met Gly Arg Thr Val Gly Ile Asn Thr Arg Ile Asp Phe

660

665

670

Phe

<210> 3

<211> 246

<212> PRT

<213> Escherichia coli

<400> 3

Met Asn Lys Val Phe Val Val Ser Val Val Ala Ala Ala Cys Val Phe
 1 5 10 15

Ala Val Asn Ala Gly Ala Lys Glu Gly Lys Ser Gly Phe Tyr Leu Thr
 20 25 30

Gly Lys Ala Gly Ala Ser Val Met Ser Leu Ser Asp Gln Arg Phe Leu
 35 40 45

Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His
 50 55 60

Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro
 65 70 75 80

Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly
 85 90 95

Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly
 100 105 110

Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met
 115 120 125

Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp
 130 135 140

Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly
 145 150 155 160

Ile Ser Thr Trp Asp Tyr Glu Tyr Gly Ser Ser Gly Arg Glu Ser Leu
 165 170 175

Ser Arg Ser Gly Ser Ala Asp Asn Phe Ala Trp Ser Leu Gly Ala Gly
 180 185 190

Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg
 195 200 205

Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly
 210 215 220

Asp Lys Tyr Lys Ser Glu Val Asp Val Lys Ser His Asp Ile Met Leu
 225 230 235 240

Gly Met Thr Tyr Asn Phe
 245

<210> 4
 <211> 166
 <212> PRT
 <213> Escherichia coli
 <400> 4

Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile
 1 5 10 15

Ala Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Arg
 20 25 30

Val Leu Pro Arg Thr Cys Thr Ile Gly Asn Gly Gly Asn Pro Asn Ala
 35 40 45

Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn
 50 55 60

Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln
 65 70 75 80

Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn
 85 90 95

Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln
 100 105 110

Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val
 115 120 125

Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala
 130 135 140

Val Ser Lys Gly Asn Ala Gly Ala Gly Ser Ile Asn Ser Gln Ile Thr
 145 150 155 160

Val Thr Tyr Thr Tyr Ala
 165

<210> 5
 <211> 1295
 <212> PRT
 <213> Escherichia coli
 <400> 5

Met Asn Lys Ile Tyr Ser Leu Lys Tyr Ser Ala Ala Thr Gly Gly Leu
 1 5 10 15

Ile Ala Val Ser Glu Leu Ala Lys Arg Val Ser Gly Lys Thr Asn Arg
 20 25 30

Lys Leu Val Ala Thr Met Leu Ser Leu Ala Val Ala Gly Thr Val Asn
 35 40 45

Ala Ala Asn Ile Asp Ile Ser Asn Val Trp Ala Arg Asp Tyr Leu Asp
 50 55 60

Leu Ala Gln Asn Lys Gly Ile Phe Gln Pro Gly Ala Thr Asp Val Thr
 65 70 75 80

Ile Thr Leu Lys Asn Gly Asp Lys Phe Ser Phe His Asn Leu Ser Ile
 85 90 95

Pro Asp Phe Ser Gly Ala Ala Ala Ser Gly Ala Ala Thr Ala Ile Gly
 100 105 110

Gly Ser Tyr Ser Val Thr Val Ala His Asn Lys Lys Asn Pro Gln Ala
 115 120 125

Ala Glu Thr Gln Val Tyr Ala Gln Ser Ser Tyr Arg Val Val Asp Arg
 130 135 140

Arg Asn Ser Asn Asp Phe Glu Ile Gln Arg Leu Asn Lys Phe Val Val
 145 150 155 160

Glu Thr Val Gly Ala Thr Pro Ala Glu Thr Asn Pro Thr Thr Tyr Ser
 165 170 175

Asp Ala Leu Glu Arg Tyr Gly Ile Val Thr Ser Asp Gly Ser Lys Lys
 180 185 190

Ile Ile Gly Phe Arg Ala Gly Ser Gly Gly Thr Ser Phe Ile Asn Gly
 195 200 205

Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser
 210 215 220

Ala Ser Leu Phe Glu Val Thr Gln Trp Asp Ser Tyr Gly Met Met Ile
 225 230 235 240

Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser
 245 250 255

Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu
 260 265 270

Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr
 275 280 285

Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr
 290 295 300

Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn
 305 310 315 320

Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln
 325 330 335

Glu Lys Ile Thr Lys Asp Lys Asp Ile Val Phe Thr Asn Gly Gly Asp
 340 345 350

Val Leu Phe Lys Asp Asn Leu Asp Phe Gly Ser Gly Gly Ile Ile Phe
 355 360 365

Asp Glu Gly His Glu Tyr Asn Ile Asn Gly Gln Gly Phe Thr Phe Lys
 370 375 380

Gly Ala Gly Ile Asp Ile Gly Lys Glu Ser Ile Val Asn Trp Asn Ala
 385 390 395 400

Leu Tyr Ser Ser Asp Asp Val Leu His Lys Ile Gly Pro Gly Thr Leu
 405 410 415

Asn Val Gln Lys Lys Gln Gly Ala Asn Ile Lys Ile Gly Glu Gly Asn
 420 425 430

Val Ile Leu Asn Glu Glu Gly Thr Phe Asn Asn Ile Tyr Leu Ala Ser
 435 440 445

Gly Asn Gly Lys Val Ile Leu Asn Lys Asp Asn Ser Leu Gly Asn Asp
 450 455 460

Gln Tyr Ala Gly Ile Phe Phe Thr Lys Arg Gly Gly Thr Leu Asp Leu
 465 470 475 480

Asn Gly His Asn Gln Thr Phe Thr Arg Ile Ala Ala Thr Asp Asp Gly
 485 490 495

Thr Thr Ile Thr Asn Ser Asp Thr Thr Lys Glu Ala Val Leu Ala Ile
 500 505 510

Asn Asn Glu Asp Ser Tyr Ile Tyr His Gly Asn Ile Asn Gly Asn Ile
 515 520 525

Lys Leu Thr His Asn Ile Asn Ser Gln Asp Lys Lys Thr Asn Ala Lys
 530 535 540

Leu Ile Leu Asp Gly Ser Val Asn Thr Lys Asn Asp Val Glu Val Ser
 545 550 555 560

Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe
 565 570 575

Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp
 580 585 590

Trp Val Thr Val Leu Lys Glu Thr Glu Ser Ser Tyr Asn Lys Lys Phe
 595 600 605

Asn Ser Asp Tyr Lys Ser Asn Asn Gln Gln Thr Ser Phe Asp Gln Pro
 610 615 620

Asp Trp Lys Thr Gly Val Phe Lys Phe Asp Thr Leu His Leu Asn Asn
 625 630 635 640

Ala Asp Phe Ser Ile Ser Arg Asn Ala Asn Val Glu Gly Asn Ile Ser
 645 650 655

Ala Asn Lys Ser Ala Ile Thr Ile Gly Asp Lys Asn Val Tyr Ile Asp
 660 665 670

Asn Leu Ala Gly Lys Asn Ile Thr Asn Asn Gly Phe Asp Phe Lys Gln
 675 680 685

Thr Ile Ser Thr Asn Leu Ser Ile Gly Glu Thr Lys Phe Thr Gly Gly
 690 695 700

Ile Thr Ala His Asn Ser Gln Ile Ala Ile Gly Asp Gln Ala Val Val
 705 710 715 720

Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp
 725 730 735

Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly
 740 745 750

Ile Asp Ile Ser Gly Glu Leu Thr Met Met Gly Ile Pro Glu Gln Asn
 755 760 765

Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg
 770 775 780

Leu Ser Gly Gly Asn Ala Asn Phe Ile Ala Arg Asn Met Ala Ser Val
 785 790 795 800

Thr Gly Asn Ile Tyr Ala Asp Asp Ala Ala Thr Ile Thr Leu Gly Gln
 805 810 815

Pro Glu Thr Glu Thr Pro Thr Ile Ser Ser Ala Tyr Gln Ala Trp Ala
 820 825 830

Glu Thr Leu Leu Tyr Gly Phe Asp Thr Ala Tyr Arg Gly Ala Ile Thr

835

840

845

Ala Pro Lys Ala Thr Val Ser Met Asn Asn Ala Ile Trp His Leu Asn
 850 855 860

Ser Gln Ser Ser Ile Asn Arg Leu Glu Thr Lys Asp Ser Met Val Arg
 865 870 875 880

Phe Thr Gly Asp Asn Gly Lys Phe Thr Thr Leu Thr Val Asn Asn Leu
 885 890 895

Thr Ile Asp Asp Ser Ala Phe Val Leu Arg Ala Asn Leu Ala Gln Ala
 900 905 910

Asp Gln Leu Val Val Asn Lys Ser Leu Ser Gly Lys Asn Asn Leu Leu
 915 920 925

Leu Val Asp Phe Ile Glu Lys Asn Gly Asn Ser Asn Gly Leu Asn Ile
 930 935 940

Asp Leu Val Ser Ala Pro Lys Gly Thr Ala Val Asp Val Phe Lys Ala
 945 950 955 960

Thr Thr Arg Ser Ile Gly Phe Ser Asp Val Thr Pro Val Ile Glu Gln
 965 970 975

Lys Asn Asp Thr Asp Lys Ala Thr Trp Thr Leu Ile Gly Tyr Lys Ser
 980 985 990

Val Ala Asn Ala Asp Ala Ala Lys Lys Ala Thr Leu Leu Met Ser Gly
 995 1000 1005

Gly Tyr Lys Ala Phe Leu Ala Glu Val Asn Asn Leu Asn Lys Arg
 1010 1015 1020

Met Gly Asp Leu Arg Asp Ile Asn Gly Glu Ser Gly Ala Trp Ala
 1025 1030 1035

Arg Ile Ile Ser Gly Thr Gly Ser Ala Gly Gly Gly Phe Ser Asp
 1040 1045 1050

Asn Tyr Thr His Val Gln Val Gly Ala Asp Asn Lys His Glu Leu
 1055 1060 1065

Asp Gly Leu Asp Leu Phe Thr Gly Val Thr Met Thr Tyr Thr Asp
 1070 1075 1080

Ser His Ala Gly Ser Asp Ala Phe Ser Gly Glu Thr Lys Ser Val
 1085 1090 1095

Gly Ala Gly Leu Tyr Ala Ser Ala Met Phe Glu Ser Gly Ala Tyr
 1100 1105 1110

Ile Asp Leu Ile Gly Lys Tyr Val His His Asp Asn Glu Tyr Thr
 1115 1120 1125

Ala Thr Phe Ala Gly Leu Gly Thr Arg Asp Tyr Ser Ser His Ser
 1130 1135 1140

Trp Tyr Ala Gly Ala Glu Val Gly Tyr Arg Tyr His Val Thr Asp
 1145 1150 1155

Ser Ala Trp Ile Glu Pro Gln Ala Glu Leu Val Tyr Gly Ala Val
 1160 1165 1170

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr
 1175 1180 1185

Met Lys Asp Lys Asp Phe Asn Pro Leu Ile Gly Arg Thr Gly Val
 1190 1195 1200

Asp Val Gly Lys Ser Phe Ser Gly Lys Asp Trp Lys Val Thr Ala
 1205 1210 1215

Arg Ala Gly Leu Gly Tyr Gln Phe Asp Leu Phe Ala Asn Gly Glu
 1220 1225 1230

Thr Val Leu Arg Asp Ala Ser Gly Glu Lys Arg Ile Lys Gly Glu
 1235 1240 1245

Lys Asp Gly Arg Met Leu Met Asn Val Gly Leu Asn Ala Glu Ile
 1250 1255 1260

Arg Asp Asn Leu Arg Phe Gly Leu Glu Phe Glu Lys Ser Ala Phe
 1265 1270 1275

Gly Lys Tyr Asn Val Asp Asn Ala Ile Asn Ala Asn Phe Arg Tyr
 1280 1285 1290

Ser Phe
 1295

<210> 6
 <211> 142
 <212> PRT
 <213> Escherichia coli
 <400> 6

Met Ile Asn Ile Pro Ser Pro Thr Ala Val Val Met Ala Leu Val Ala
 1 5 10 15

Ile Ser Thr Leu Pro Ser Pro Ser Arg Val Lys Leu Met Pro Tyr Pro
 20 25 30

Pro Arg Ala His Asn Thr Thr Gly Leu Leu Pro Val Arg Glu Ile Cys
 35 40 45

Phe Pro His His Gly Asp Asp Gly Arg Asn Ser Ile Glu Pro Ser Ile
 50 55 60

Ser Arg Ala Ala His Thr Asp Arg Leu Arg Phe Val Cys Met Thr Arg
 65 70 75 80

Thr Gly Ser Thr Thr Ser Arg Pro Phe Cys Pro Ile Pro Arg Ser Pro
 85 90 95

Ala Leu Asn Ala Ser Gly Gln Gln Asp Ser Gly Phe Trp Gly Val Ser
 100 105 110

Ser Ile Pro Gly Asp Ile Leu Met Phe Gln Leu His Val Leu Ile Val
 115 120 125

Phe Ile Cys Lys Ile Asn Leu Ser Asp Asn Asn Ile Ser Tyr
 130 135 140

<210> 7
 <211> 318
 <212> PRT
 <213> Escherichia coli
 <400> 7

14

Met Tyr Ala Arg Glu Tyr Arg Ser Thr Arg Pro His Lys Ala Ile Phe
 1 5 10 15

Phe His Leu Ser Cys Leu Thr Leu Ile Cys Ser Ala Gln Val Tyr Ala
 20 25 30

Lys Pro Asp Met Arg Pro Leu Gly Pro Asn Ile Ala Asp Lys Gly Ser
 35 40 45

Val Phe Tyr His Phe Ser Ala Thr Ser Phe Asp Ser Val Asp Gly Thr
 50 55 60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
 65 70 75 80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
 85 90 95

Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro
 100 105 110

Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn
 115 120 125

Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
 130 135 140

Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
 145 150 155 160

Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
 165 170 175

Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
 180 185 190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
 195 200 205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
 210 215 220

Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Thr Lys His Leu Ala

Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Ile Asp Gly Val
100 105 110

Pro Val Thr Ser Arg Asn Ser Val Arg Tyr Ser Trp Arg Gly Glu Arg
 115 120 125

Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg
 130 135 140

Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala
 145 150 155 160

Ala Gly Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asn Asp Trp
 165 170 175

His Gly Ser Leu Ser Leu Tyr Thr Asn Gln Pro Glu Ser Ser Glu Glu
 180 185 190

Gly Ala Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Ala Gly
 195 200 205

Asp Ala Leu Thr Thr Arg Leu Tyr Gly Asn Leu Asn Lys Thr Asp Ala
 210 215 220

Asp Ser Trp Asp Ile Asn Ser Pro Val Gly Thr Lys Asn Ala Ala Gly
 225 230 235 240

His Glu Gly Val Arg Asn Lys Asp Ile Asn Gly Val Val Ser Trp Lys
 245 250 255

Leu Asn Pro Gln Gln Ile Leu Asp Phe Glu Val Gly Tyr Ser Arg Gln
 260 265 270

Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Ser Ser Ser Ser Ala Val
 275 280 285

Thr Glu Ser Leu Ala Lys Ser Gly Lys Glu Thr Asn Arg Leu Tyr Arg
 290 295 300

Gln Asn Tyr Gly Ile Thr His Asn Gly Ile Trp Asp Trp Gly Gln Ser
 305 310 315 320

Arg Phe Gly Val Tyr Tyr Glu Lys Thr Asn Asn Thr Arg Met Asn Glu
 325 330 335

Gly Leu Ser Gly Gly Gly Glu Gly Arg Ile Leu Ala Gly Glu Lys Phe

340

345

350

Thr Thr Asn Arg Leu Ser Ser Trp Arg Thr Ser Gly Glu Leu Asn Ile
 355 360 365

Pro Leu Asn Val Met Val Asp Gln Thr Leu Thr Val Gly Ala Glu Trp
 370 375 380

Asn Arg Asp Lys Leu Asp Asp Pro Ser Ser Thr Ser Leu Thr Val Asn
 385 390 395 400

Asp Arg Asp Ile Ser Gly Ile Ser Gly Ser Ala Ala Asp Arg Ser Ser
 405 410 415

Lys Asn His Ser Gln Ile Ser Ala Leu Tyr Ile Glu Asp Asn Ile Glu
 420 425 430

Pro Val Pro Gly Thr Asn Ile Ile Pro Gly Leu Arg Phe Asp Tyr Leu
 435 440 445

Ser Asp Ser Gly Gly Asn Phe Ser Pro Ser Leu Asn Leu Ser Gln Glu
 450 455 460

Leu Gly Asp Tyr Phe Lys Val Lys Ala Gly Val Ala Arg Thr Phe Lys
 465 470 475 480

Ala Pro Asn Leu Tyr Gln Ser Ser Glu Gly Tyr Leu Leu Tyr Ser Lys
 485 490 495

Gly Asn Gly Cys Pro Lys Asp Ile Thr Ser Gly Gly Cys Tyr Leu Ile
 500 505 510

Gly Asn Lys Asp Leu Asp Pro Glu Ile Ser Val Asn Lys Glu Ile Gly
 515 520 525

Leu Glu Phe Thr Trp Glu Asp Tyr His Ala Ser Val Thr Tyr Phe Arg
 530 535 540

Asn Asp Tyr Gln Asn Lys Ile Val Ala Gly Asp Asn Val Ile Gly Gln
 545 550 555 560

Thr Ala Ser Gly Ala Tyr Ile Leu Lys Trp Gln Asn Gly Gly Lys Ala
 565 570 575

Leu Val Asp Gly Ile Glu Ala Ser Met Ser Phe Pro Leu Val Lys Glu
 580 585 590

Arg Leu Asn Trp Asn Thr Asn Ala Thr Trp Met Ile Thr Ser Glu Gln
 595 600 605

Lys Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Lys Tyr Thr Ile Asn
 610 615 620

Asn Ser Leu Asn Trp Thr Ile Thr Gln Ala Phe Ser Ala Ser Phe Asn
 625 630 635 640

Trp Thr Leu Tyr Gly Arg Gln Lys Pro Arg Thr His Ala Glu Thr Arg
 645 650 655

Ser Glu Asp Thr Gly Gly Leu Ser Gly Lys Glu Leu Gly Ala Tyr Ser
 660 665 670

Leu Val Gly Thr Asn Phe Asn Tyr Asp Ile Asn Lys Asn Leu Arg Leu
 675 680 685

Asn Val Gly Val Ser Asn Ile Leu Asn Lys Gln Ile Phe Arg Ser Ser
 690 695 700

Glu Gly Ala Asn Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Gly
 705 710 715 720

Val Thr Ala Ser Phe
 725

<210> 9
 <211> 1014
 <212> PRT
 <213> Escherichia coli
 <400> 9

Met Gly Asn Gln Trp Gln Gln Lys Tyr Leu Leu Glu Tyr Asn Glu Leu
 1 5 10 15

Val Ser Asn Phe Pro Ser Pro Glu Arg Val Val Ser Asp Tyr Ile Lys
 20 25 30

Asn Cys Phe Lys Thr Asp Leu Pro Trp Phe Ser Arg Ile Asp Pro Asp

35 40 45
 Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser
 50 55 60
 Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr
 65 70 75 80
 Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe
 85 90 95
 Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp
 100 105 110
 Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu
 115 120 125
 His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu
 130 135 140
 Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys
 145 150 155 160
 Asn Tyr Tyr Ile Ser Ser Ala Leu Tyr Leu Tyr Lys Asn Gly Glu Leu
 165 170 175
 Asp Glu Arg Glu Tyr Asn Phe Ser Met Asn Ala Leu Asn Arg Ser Asp
 180 185 190
 Asn Ile Ser Leu Leu Phe Phe Asp Ile Tyr Gly Tyr Tyr Ala Ser Asp
 195 200 205
 Ile Phe Val Ala Lys Asn Asn Asp Lys Val Met Leu Phe Ile Pro Gly
 210 215 220
 Ala Lys Lys Pro Phe Leu Phe Lys Lys Asn Ile Ala Asp Leu Arg Leu
 225 230 235 240
 Thr Leu Lys Glu Leu Ile Lys Asp Ser Asp Asn Lys Gln Leu Leu Ser
 245 250 255
 Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Val Ser Tyr Ala Gly
 260 265 270

Val Asn Ser Val Leu His Ala Ile Glu Asn Asp Gly Asn Phe Asn Glu
 275 280 285

Ser Tyr Phe Leu Tyr Ser Asn Lys Thr Leu Ser Asn Lys Asp Val Phe
 290 295 300

Asp Ala Ile Ala Ile Ser Val Lys Lys Arg Ser Phe Ser Asp Gly Asp
 305 310 315 320

Ile Val Ile Lys Ser Asn Ser Glu Ala Gln Arg Asp Tyr Ala Leu Thr
 325 330 335

Ile Leu Gln Thr Ile Leu Ser Met Thr Pro Ile Phe Asp Ile Val Val
 340 345 350

Pro Glu Val Ser Val Pro Leu Gly Leu Gly Ile Ile Thr Ser Ser Met
 355 360 365

Gly Ile Ser Phe Asp Gln Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg
 370 375 380

Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Ala Val Leu Leu Gly Leu
 385 390 395 400

Ser Phe Ala Ile Pro Leu Leu Ile Ser Lys Ala Gly Ile Asn Gln Glu
 405 410 415

Val Leu Ser Ser Val Ile Asn Asn Glu Gly Arg Thr Leu Asn Glu Thr
 420 425 430

Asn Ile Asp Ile Phe Leu Lys Glu Tyr Gly Ile Ala Glu Asp Ser Ile
 435 440 445

Ser Ser Thr Asn Leu Leu Asp Val Lys Leu Lys Ser Ser Gly Gln His
 450 455 460

Val Asn Ile Val Lys Leu Ser Asp Glu Asp Asn Gln Ile Val Ala Val
 465 470 475 480

Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr
 485 490 495

Gly Tyr Glu Ile Leu Ser Arg Arg Ile Tyr Arg Thr Glu Tyr Asn Asn
 500 505 510

Glu Ile Leu Trp Thr Arg Gly Gly Gly Leu Lys Gly Gly Gln Pro Phe
 515 520 525

Asp Phe Glu Ser Leu Asn Ile Pro Val Phe Phe Lys Asp Glu Pro Tyr
 530 535 540

Ser Ala Val Thr Gly Ser Pro Leu Ser Phe Ile Asn Asp Asp Ser Ser
 545 550 555 560

Leu Leu Tyr Pro Asp Thr Asn Pro Lys Leu Pro Gln Pro Thr Ser Glu
 565 570 575

Met Asp Ile Val Asn Tyr Val Lys Gly Ser Gly Ser Phe Gly Asp Arg
 580 585 590

Phe Val Thr Leu Met Arg Gly Ala Thr Glu Glu Glu Ala Trp Asn Ile
 595 600 605

Ala Ser Tyr His Thr Ala Gly Gly Ser Thr Glu Glu Leu His Glu Ile
 610 615 620

Leu Leu Gly Gln Gly Pro Gln Ser Ser Leu Gly Phe Thr Glu Tyr Thr
 625 630 635 640

Ser Asn Val Asn Ser Ala Asp Ala Ala Ser Arg Arg His Phe Leu Val
 645 650 655

Val Ile Lys Val His Val Lys Tyr Ile Thr Asn Asn Asn Val Ser Tyr
 660 665 670

Val Asn His Trp Ala Ile Pro Asp Glu Ala Pro Val Glu Val Leu Ala
 675 680 685

Val Val Asp Arg Arg Phe Asn Phe Pro Glu Pro Ser Thr Pro Pro Asp
 690 695 700

Ile Ser Thr Ile Arg Lys Leu Leu Ser Leu Arg Tyr Phe Lys Glu Ser
 705 710 715 720

Ile Glu Ser Thr Ser Lys Ser Asn Phe Gln Lys Leu Ser Arg Gly Asn
 725 730 735

Ile Asp Val Leu Lys Gly Arg Gly Ser Ile Ser Ser Thr Arg Gln Arg
 740 745 750

Ala Ile Tyr Pro Tyr Phe Glu Ala Ala Asn Ala Asp Glu Gln Gln Pro
 755 760 765

Leu Phe Phe Tyr Ile Lys Lys Asp Arg Phe Asp Asn His Gly Tyr Asp
 770 775 780

Gln Tyr Phe Tyr Asp Asn Thr Val Gly Leu Asn Gly Ile Pro Thr Leu
 785 790 795 800

Asn Thr Tyr Thr Gly Glu Ile Pro Ser Asp Ser Ser Ser Leu Gly Ser
 805 810 815

Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg
 820 825 830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu
 835 840 845

Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser
 850 855 860

Gly Cys Thr Thr Ile Val Ala Arg Lys Glu Gly Tyr Ile Tyr Lys Val
 865 870 875 880

His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly
 885 890 895

Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile
 900 905 910

Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu
 915 920 925

Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys
 930 935 940

Lys Pro Asp Ser Gln Ile Thr Ile Ile Arg Asp Asn Val Ser Val Phe

23

945 950 955 960
 Pro Tyr Phe Leu Asp Asn Ile Pro Glu His Gly Phe Gly Thr Ser Ala
 965 970 975
 Thr Val Leu Val Arg Val Asp Gly Asn Val Val Val Arg Ser Leu Ser
 980 985 990
 Glu Ser Tyr Ser Leu Asn Ala Asp Ala Ser Glu Ile Ser Val Leu Lys
 995 1000 1005
 Val Phe Ser Lys Lys Phe
 1010

 <210> 10
 <211> 454
 <212> PRT
 <213> Escherichia coli
 <400> 10

 Met Val Asp Met Ile Asn Glu Ser Ala Arg Gln Thr Pro Val Ile Ala
 1 5 10 15

 Gln Thr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala
 20 25 30

 Ala Ile Ala Ala Gly Arg Leu Gly Ala Arg Thr Met Ile Val Glu Arg
 35 40 45

 Tyr Gly Ser Leu Gly Gly Val Leu Thr Gln Val Gly Val Glu Ser Phe
 50 55 60

 Ala Trp Tyr Arg His Pro Gly Thr Glu Asp Cys Glu Gly Ile Cys Arg
 65 70 75 80

 Glu Tyr Glu Gly Arg Ala Arg Ala Leu Gly Phe Thr Arg Pro Glu Pro
 85 90 95

 Gln Ser Ile Ser Glu Val Ile Asp Thr Glu Gly Phe Lys Val Val Ala
 100 105 110

 Asp Gln Met Ile Thr Glu Ser Gly Val Glu Pro Leu Tyr His Ser Trp
 115 120 125

Val Val Asp Val Ile Lys Asp Gly Asp Thr Leu Cys Gly Val Ile Val
 130 135 140

Glu Asn Lys Ser Gly Arg Gly Ala Ile Leu Ala Lys Arg Ile Val Asp
 145 150 155 160

Cys Thr Gly Asp Ala Asp Ile Ala Ala Arg Ala Gly Ala Pro Trp Thr
 165 170 175

Lys Arg Ser Lys Asp Gln Leu Met Gly Val Thr Val Met Phe Ser Cys
 180 185 190

Ala Gly Val Asp Val Ala Arg Phe Asn Arg Phe Val Ala Glu Glu Leu
 195 200 205

Lys Pro Thr Tyr Ala Asp Trp Gly Lys Asn Trp Thr Ile Gln Thr Thr
 210 215 220

Gly Lys Glu Asp Pro Met Phe Ser Pro Tyr Met Glu Asp Ile Phe Thr
 225 230 235 240

Arg Ala Gln Gln Asp Gly Val Ile Pro Gly Asp Ala Gln Ala Ile Ala
 245 250 255

Gly Thr Trp Ser Thr Phe Ser Glu Ser Gly Glu Ala Phe Gln Met Asn
 260 265 270

Met Val Tyr Ala Phe Gly Phe Asp Cys Thr Asp Val Phe Asp Leu Thr
 275 280 285

Lys Ala Glu Ile Ala Gly Arg Gln Gln Ala Leu Trp Ala Ile Asp Ala
 290 295 300

Leu Arg His Tyr Val Pro Gly Phe Glu Asn Val Arg Leu Arg Asn Phe
 305 310 315 320

Gly Ala Thr Leu Gly Thr Arg Glu Ser Arg Leu Ile Glu Gly Glu Ile
 325 330 335

Arg Ile Ala Asp Asp Tyr Val Leu Asn Gln Gly Arg Cys Ser Asp Ser
 340 345 350

Val Gly Ile Phe Pro Glu Phe Ile Asp Gly Ser Gly Tyr Leu Ile Leu

355

360

365

Pro Thr Thr Gly Arg Phe Phe Gln Ile Pro Tyr Gly Cys Leu Val Pro
 370 375 380

Gln Lys Val Glu Asn Leu Leu Val Ala Gly Arg Cys Ile Ser Ala Gly
 385 390 395 400

Val Val Ala His Thr Ser Met Arg Asn Met Met Cys Cys Ala Val Thr
 405 410 415

Gly Glu Ala Ala Gly Thr Ala Ala Val Val Ser Leu Gln Gln Asn Cys
 420 425 430

Thr Val Arg Gln Val Ala Ile Pro Asp Leu Gln Asn Thr Leu Gln Gln
 435 440 445

Gln Gly Val Arg Leu Ala
 450

<210> 11

<211> 253

<212> PRT

<213> Escherichia coli

<400> 11

Met Ser Ala Lys Arg Arg Leu Leu Ile Ala Cys Thr Leu Ile Thr Ala
 1 5 10 15

Ile Tyr His Phe Pro Ala Tyr Ser Ser Leu Glu Tyr Lys Gly Thr Phe
 20 25 30

Gly Ser Ile Asn Ala Gly Tyr Ala Asp Trp Asn Ser Gly Phe Val Asn
 35 40 45

Thr His Arg Gly Glu Val Trp Lys Val Thr Ala Asp Phe Gly Val Asn
 50 55 60

Phe Lys Glu Ala Glu Phe Tyr Ser Phe Tyr Glu Ser Asn Val Leu Asn
 65 70 75 80

His Ala Val Ala Gly Arg Asn His Thr Val Ser Ala Met Thr His Val
 85 90 95

Arg Leu Phe Asp Ser Asp Met Thr Phe Phe Gly Lys Ile Tyr Gly Gln
 100 105 110

Trp Asp Asn Ser Trp Gly Asp Asp Leu Asp Met Phe Tyr Gly Phe Gly
 115 120 125

Tyr Leu Gly Trp Asn Gly Glu Trp Gly Phe Phe Lys Pro Tyr Ile Gly
 130 135 140

Leu His Asn Gln Ser Gly Asp Tyr Val Ser Ala Lys Tyr Gly Gln Thr
 145 150 155 160

Asn Gly Trp Asn Gly Tyr Val Val Gly Trp Thr Ala Val Leu Pro Phe
 165 170 175

Thr Leu Phe Asp Glu Lys Phe Val Leu Ser Asn Trp Asn Glu Ile Glu
 180 185 190

Leu Asp Arg Asn Asp Ala Tyr Thr Glu Gln Gln Phe Gly Arg Asn Gly
 195 200 205

Leu Asn Gly Gly Leu Thr Ile Ala Trp Lys Phe Tyr Pro Arg Trp Lys
 210 215 220

Ala Ser Val Thr Trp Arg Tyr Phe Asp Asn Lys Leu Gly Tyr Asp Gly
 225 230 235 240

Phe Gly Asp Gln Met Ile Tyr Met Leu Gly Tyr Asp Phe
 245 250

<210> 12
 <211> 492
 <212> PRT
 <213> Escherichia coli
 <400> 12

Met Ala Ser Leu Ile Gly Leu Ala Val Cys Thr Gly Asn Ala Phe Ser
 1 5 10 15

Pro Ala Leu Ala Ala Glu Ala Lys Gln Pro Asn Leu Val Ile Ile Met
 20 25 30

Ala Asp Asp Leu Gly Tyr Gly Asp Leu Ala Thr Tyr Gly His Gln Ile
 35 40 45

Val Lys Thr Pro Asn Ile Asp Arg Leu Ala Gln Glu Gly Val Lys Phe
 50 55 60

Thr Asp Tyr Tyr Ala Pro Ala Pro Leu Ser Ser Pro Ser Arg Ala Gly
 65 70 75 80

Leu Leu Thr Gly Arg Met Pro Phe Arg Thr Gly Ile Arg Ser Trp Ile
 85 90 95

Pro Ser Gly Lys Asp Val Ala Leu Gly Arg Asn Glu Leu Thr Ile Ala
 100 105 110

Asn Leu Leu Lys Ala Gln Gly Tyr Asp Thr Ala Met Met Gly Lys Leu
 115 120 125

His Leu Asn Ala Gly Gly Asp Arg Thr Asp Gln Pro Gln Ala Gln Asp
 130 135 140

Met Gly Phe Asp Tyr Ser Leu Ala Asn Thr Ala Gly Phe Val Thr Asp
 145 150 155 160

Ala Thr Leu Asp Asn Ala Lys Glu Arg Pro Arg Tyr Gly Met Val Tyr
 165 170 175

Pro Thr Gly Trp Leu Arg Asn Gly Gln Pro Thr Pro Arg Ala Asp Lys
 180 185 190

Met Ser Gly Glu Tyr Val Ser Ser Glu Val Val Asn Trp Leu Asp Asn
 195 200 205

Lys Lys Asp Ser Lys Pro Phe Phe Leu Tyr Val Ala Phe Thr Glu Val
 210 215 220

His Ser Pro Leu Ala Ser Pro Lys Lys Tyr Leu Asp Met Tyr Ser Gln
 225 230 235 240

Tyr Met Ser Ala Tyr Gln Lys Gln His Pro Asp Leu Phe Tyr Gly Asp
 245 250 255

Trp Ala Asp Lys Pro Trp Arg Gly Val Gly Glu Tyr Tyr Ala Asn Ile
 260 265 270

Ser Tyr Leu Asp Ala Gln Val Gly Lys Val Leu Asp Lys Ile Lys Ala
 275 280 285

Met Gly Glu Glu Asp Asn Thr Ile Val Ile Phe Thr Ser Asp Asn Gly
 290 295 300

Pro Val Thr Arg Glu Ala Arg Lys Val Tyr Glu Leu Asn Leu Ala Gly
 305 310 315 320

Glu Thr Asp Gly Leu Arg Gly Arg Lys Asp Asn Leu Trp Glu Gly Gly
 325 330 335

Ile Arg Val Pro Ala Ile Ile Lys Tyr Gly Lys His Leu Pro Gln Gly
 340 345 350

Met Val Ser Asp Thr Pro Val Tyr Gly Leu Asp Trp Met Pro Thr Leu
 355 360 365

Ala Lys Met Met Asn Phe Lys Leu Pro Thr Asp Arg Thr Phe Asp Gly
 370 375 380

Glu Ser Leu Val Pro Val Leu Glu Gln Lys Ala Leu Lys Arg Glu Lys
 385 390 395 400

Pro Leu Ile Phe Gly Ile Asp Met Pro Phe Gln Asp Asp Pro Thr Asp
 405 410 415

Glu Trp Ala Ile Arg Asp Gly Asp Trp Lys Met Ile Ile Asp Arg Asn
 420 425 430

Asn Lys Pro Lys Tyr Leu Tyr Asn Leu Lys Ser Asp Arg Tyr Glu Thr
 435 440 445

Leu Asn Leu Ile Gly Lys Lys Pro Asp Ile Glu Lys Gln Met Tyr Gly
 450 455 460

Lys Phe Leu Lys Tyr Lys Thr Asp Ile Asp Asn Asp Ser Leu Met Lys
 465 470 475 480

Ala Arg Gly Asp Lys Pro Glu Ala Val Thr Trp Gly
 485 490

<211> 345
 <212> PRT
 <213> Escherichia coli
 <400> 13

Leu Ile Ser Leu Ser Phe Ile Pro Val Met Ser Ala Leu Pro Gly Pro
 1 5 10 15

Ile Ala Lys Gly Phe Arg Asn Glu Arg Gly Phe Val Thr Thr Thr Ile
 20 25 30

Cys Ala Met Gly Glu Leu Leu Ala Glu Phe Leu Ser Arg Asn Pro His
 35 40 45

Gln Lys Phe Thr Gln Pro Gly Glu Phe Ile Gly Pro Phe Pro Ser Gly
 50 55 60

Ala Pro Ala Ile Phe Ala Ala Gln Val Ala Lys Leu Ser His Arg Ala
 65 70 75 80

Ile Phe Phe Gly Cys Val Gly Asn Asp Asp Phe Ala Arg Leu Ile Ile
 85 90 95

Glu Arg Leu Arg His Glu Gly Val Ile Thr Asp Gly Ile His Val Met
 100 105 110

Asn Asn Ala Val Thr Gly Thr Ala Phe Val Ser Tyr Gln Asn Pro Gln
 115 120 125

Gln Arg Asp Phe Val Phe Asn Ile Pro Asn Ser Ala Cys Gly Leu Phe
 130 135 140

Thr Ala Glu His Ile Asp Lys Asp Leu Leu Lys Gln Cys Asn His Leu
 145 150 155 160

His Ile Val Gly Ser Ser Leu Phe Ser Phe Arg Met Ile Asp Val Met
 165 170 175

Arg Lys Ala Ile Thr Thr Ile Lys Ser Ala Gly Gly Thr Val Ser Phe
 180 185 190

Asp Pro Asn Ile Arg Lys Glu Met Leu Ser Ile Pro Glu Met Ala Gln
 195 200 205

30

Ala Leu Asp Tyr Leu Ile Glu Tyr Thr Asp Ile Phe Ile Pro Ser Glu
 210 215 220

Ser Glu Leu Pro Phe Phe Ala Arg His Lys Asn Leu Ser Glu Glu Gln
 225 230 235 240

Ile Val Ser Asp Leu Leu His Gly Gly Val Lys His Val Ala Ile Lys
 245 250 255

Arg Ala Gln Arg Gly Ala Ser Tyr Tyr Lys Leu Lys Asn Gly Thr Leu
 260 265 270

His Ala Gln His Val Ala Gly His Asp Ile Glu Ile Ile Asp Pro Thr
 275 280 285

Gly Ala Gly Asp Cys Phe Gly Ala Thr Phe Ile Thr Leu Phe Leu Ser
 290 295 300

Gly Phe Pro Ala His Lys Ala Leu Gln Tyr Ala Asn Ala Ser Gly Ala
 305 310 315 320

Leu Ala Val Met Arg Gln Gly Pro Met Glu Gly Ile Ser Ser Leu Ala
 325 330 335

Asp Ile Glu Asp Phe Leu Gln Gln His
 340 345

<210> 14

<211> 192

<212> PRT

<213> Escherichia coli

<400> 14

Met Tyr Met Pro Gly Lys Gln Met Leu Cys Cys Ile Leu Ile Ser Ile
 1 5 10 15

Ile Ser Glu Gly Asp Met Lys Ile Phe Ile Ser Leu Phe Leu Phe Ile
 20 25 30

Ile Ser Thr Asn Ser Phe Ala Asp Asp Ile Thr His Ala Gly Val Val
 35 40 45

Arg Ile Glu Gly Leu Ile Thr Glu Lys Thr Cys Ile Ile Ser Asp Glu
 50 55 60

Ser Lys Asn Phe Thr Val Asn Met Pro Asp Val Pro Ser Ser Ser Val
65 70 75 80

Arg Ser Ala Gly Asp Val Thr Glu Lys Val Tyr Phe Ser Ile Thr Leu
85 90 95

Thr Arg Cys Gly Ser Asp Val Gly Asn Ala Tyr Ile Lys Phe Thr Gly
100 105 110

Asn Thr Val Ser Glu Asp Ala Ser Leu Tyr Lys Leu Glu Asp Gly Ser
115 120 125

Val Glu Gly Leu Ala Leu Thr Ile Phe Asp Lys Asn Lys Gly Ser Ile
130 135 140

Ser Asn Asp Val Lys Ser Met Val Phe Ser Leu Thr Ser Ser Val Asp
145 150 155 160

Asn Ile Leu His Phe Phe Ala Ala Tyr Lys Ala Leu Lys Asn Asn Val
165 170 175

Gln Pro Gly Asp Ala Asn Ala Ser Val Ser Phe Ile Val Thr Tyr Asp
180 185 190

<210> 15
<211> 201
<212> PRT
<213> Escherichia coli
<400> 15

Met Ile Lys Phe Arg Leu Tyr Ile Pro Pro Val Ile Leu Gly Phe Val
1 5 10 15

Ile Val Pro Leu Leu Val Trp Pro Thr Val Ile Ala Leu Ala Val Leu
20 25 30

Ile Phe Thr Leu Thr Phe Leu Ala Glu Ile Ile Phe Ser Phe Pro Leu
35 40 45

Leu Val Val Arg Ile Ser Leu Gln Glu Leu Gln Leu Glu Leu Leu Val
50 55 60

Val Tyr Ala Leu Phe Phe Ser Val Met Gly Gly Ile Gly Trp Gln Phe
65 70 75 80

Ser Arg Arg Thr Pro Pro Glu Leu Lys Asn Arg Leu His Cys Trp Leu
85 90 95

Val Phe Ser Pro Val Tyr Phe Trp Leu Ile Leu Ser Asn Phe Ile Leu
100 105 110

Tyr Ile Ser Pro Glu Lys Ser Ala Leu Leu Glu Asn Ile Arg Asn Phe
115 120 125

Phe Leu Thr Phe Val Trp Leu Pro Leu Asn Phe Ser Pro Phe Trp Pro
130 135 140

Gln Pro Trp Thr Asp Phe Val Gly Pro Ile Ser Ala Gln Leu Gly Phe
145 150 155 160

Ala Leu Gly Tyr Tyr Cys Gln Trp Arg Ser Lys Asn Arg Ser His Arg
165 170 175

Lys Lys Trp Gly Asp Trp Val Thr Cys Leu Ser Leu Ala Ile Leu Ala
180 185 190

Leu Gly Pro Leu Phe Asn Tyr Leu Gln
195 200

<210> 16
<211> 234
<212> PRT
<213> Escherichia coli
<400> 16

Met Lys Phe Asn Leu Ser Asn Leu Ser Ala Val Leu Leu Ala Ser Gly
1 5 10 15

Met Leu Met Ser Thr Ala Val Thr Ala Ala Pro Gly Asp Ala Thr Gln
20 25 30

Phe Gly Gly Ala Asp Thr Asp Trp Ser Thr Val Asp Tyr Pro Arg Leu
35 40 45

Thr Asp Met Asp Asp Asn Val Asp Ser Met Gly Gly Lys Ile Arg Phe
50 55 60

Thr Gly Arg Val Val Lys Ala Thr Cys Lys Val Ala Thr Asp Ser Lys

33

65

70

75

80

Gln Ile Glu Val Val Leu Pro Val Val Pro Ser Asn Leu Phe Thr Gly
 85 90 95

Ile Asp Val Glu Ala Gln Gly Ala Ser Asn Gln Thr Asp Phe Asn Ile
 100 105 110

Asn Leu Thr Glu Cys Ser Asn Thr Asp Asp Gln Lys Ile Glu Phe Arg
 115 120 125

Phe Thr Gly Thr Ala Asp Ser Ala Asn Lys Thr Leu Ala Asn Glu Val
 130 135 140

Glu Gly Ser Thr Asp Ala Asp Asn Ser Gly Asn Ala Gly Ala Thr Gly
 145 150 155 160

Val Gly Ile Arg Ile Tyr Ser Lys Gly Thr Thr Asn Asn Gly Leu Ile
 165 170 175

Asn Leu Asn Thr Thr Ala Ala Glu Gly Ser Ala Ser Thr Ala Ala Tyr
 180 185 190

Thr Ile Pro Gly Asn Ala Thr Thr His Asp Phe Ser Ala Ala Phe Thr
 195 200 205

Ala Gly Tyr Ala Gln Asn Gly Ser Thr Val Ala Pro Gly Val Val Lys
 210 215 220

Ser Thr Ala Ser Phe Val Val Leu Tyr Glu
 225 230

<210> 17

<211> 336

<212> PRT

<213> Escherichia coli

<400> 17

Met Arg Ile His Thr Tyr Trp Tyr Arg Arg Tyr Phe Ile Leu Leu Ile
 1 5 10 15

Ile Ile Phe Ser Asn Val Leu Ser Ser Ile Ala Asn Ala Glu Asp Met
 20 25 30

34

Gly Arg Glu Arg Ala Tyr Cys Tyr Pro Gly Ser Pro Ser Asn Asn Thr
 35 40 45
 Thr Pro Ala Ser Phe Ser Tyr Asn Phe Gly Thr Ile Val Val Ser Asp
 50 55 60
 Val Asn Lys Asn Ala Pro Gly Thr Val Leu Pro Ser Gln Ile Trp Lys
 65 70 75 80
 Val Gly Thr Tyr Lys Ala Tyr Cys Asn Ser Leu Asp Asp Tyr Glu Ile
 85 90 95
 Tyr Phe Ser Ala Val Ser Gly Ile Asp Pro Ser Gly Ala Ser Gly Asp
 100 105 110
 His Gln Gly Ser Asp Val Phe Ile Pro Leu Thr His Glu Ile Ser Val
 115 120 125
 Ser Thr His Ile Lys Leu Tyr Asn Gln Asn Gly Thr Met Thr Asp Lys
 130 135 140
 Ile Val Pro Phe Glu Asn Tyr Asn Thr Asn Tyr Pro Gly Asp Arg Ser
 145 150 155 160
 Lys Pro Ser Asn Trp Ala Ser Gly Thr Glu Gly Tyr Ile Lys Ile Arg
 165 170 175
 Ile Asp Lys Lys Ile Ile Ser Asp Val Ser Leu Ser Asn Val Leu Leu
 180 185 190
 Val Ser Leu Tyr Val Ser Gln Ile Pro Thr Glu His Gly Pro Ile Pro
 195 200 205
 Val Phe Asn Ala Tyr Ile Gly Asn Leu Asn Ile Gln Val Pro Gln Gly
 210 215 220
 Cys Thr Ile Asn Glu Gly Thr Ser Phe Thr Val Asn Met Pro Asp Val
 225 230 235 240
 Trp Ala Ser Glu Leu Ser Arg Ala Gly Ala Gly Ala Lys Pro Ala Gly
 245 250 255
 Val Thr Pro Val Ala Thr Thr Ile Pro Ile Asn Cys Thr Asn Lys Asp

35

260

265

270

Thr Asp Ala Val Met Thr Leu Val Phe Asp Gly Asn Ile Ser Ala Thr
 275 280 285

Arg Asp Thr Asn Gly Lys Gln Ser Ile Ile Gln Ala Gln Asp Asn Pro
 290 295 300

Asp Val Gly Ile Met Ile Met Asp Ser Gln Gln Asn Ser Val Asp Leu
 305 310 315 320

Asn Ala Leu Ala Thr Ser Val Gly Val Pro Phe Arg Leu Val Glu Asn
 325 330 335

<210> 18
 <211> 864
 <212> PRT
 <213> Escherichia coli
 <400> 18

Met Asn Leu Lys Leu Lys Arg Cys Glu Tyr Trp Met Ala Ala Gln Lys
 1 5 10 15

Gln Met Lys Arg Val Val Pro Leu Leu Leu Val Ile Met Pro Ala Cys
 20 25 30

Ser Ile Ala Gly Met Arg Phe Asn Pro Ala Phe Leu Ser Gly Asp Thr
 35 40 45

Glu Ala Val Ala Asp Leu Ser Arg Phe Glu Lys Gly Met Thr Tyr Leu
 50 55 60

Pro Gly Ser Tyr Glu Val Glu Val Trp Val Asn Asp Ser Pro Leu Leu
 65 70 75 80

Ser Arg Thr Val Thr Phe Lys Ala Asp Asp Glu Asn Gln Leu Ile Pro
 85 90 95

Cys Leu Ser Leu Ala Asp Leu Leu Ser Leu Gly Ile Asn Lys Asn Ala
 100 105 110

Leu Pro Glu Gln Ala Leu Ala Ser Ser Glu Asn Ser Cys Leu Asp Leu
 115 120 125

Arg Ile Trp Phe Pro Asp Val His Tyr Met Pro Glu Leu Asp Ala Gln
 130 135 140

Arg Leu Lys Leu Thr Phe Pro Gln Ala Ile Ile Lys Arg Asp Ala Arg
 145 150 155 160

Gly Tyr Ile Pro Pro Glu Gln Trp Asp Asn Gly Ile Thr Ala Phe Leu
 165 170 175

Leu Asn Tyr Asp Phe Ser Gly Asn Asn Asp Arg Gly Asp Tyr Ser Ser
 180 185 190

Asn Asn Tyr Tyr Leu Asn Leu Arg Ala Gly Ile Asn Ile Gly Ala Trp
 195 200 205

Arg Phe Arg Asp Tyr Ser Thr Trp Ser Arg Gly Ser Asn Ser Ala Gly
 210 215 220

Lys Leu Glu His Ile Ser Ser Thr Leu Gln Arg Val Ile Ile Pro Phe
 225 230 235 240

Arg Ser Glu Leu Thr Leu Gly Asp Thr Trp Ser Ser Ser Asp Val Phe
 245 250 255

Asp Ser Val Ser Ile Arg Gly Ile Lys Leu Glu Ser Asp Glu Asn Met
 260 265 270

Leu Pro Asp Ser Gln Ser Gly Phe Ala Pro Thr Val Arg Gly Ile Ala
 275 280 285

Lys Ser Arg Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Val Ile Tyr
 290 295 300

Gln Thr Tyr Met Pro Pro Gly Pro Phe Glu Ile Ser Asp Leu Asn Pro
 305 310 315 320

Thr Ser Ser Ala Gly Asp Leu Glu Val Thr Ile Lys Glu Ser Asp Asn
 325 330 335

Ser Glu Thr Val Tyr Thr Val Pro Tyr Ala Ala Val Pro Ile Leu Gln
 340 345 350

Arg Glu Gly His Leu Lys Tyr Ser Thr Thr Val Gly Gln Tyr Arg Ser

355

360

365

Asn Ser Tyr Asn Gln Lys Ser Pro Tyr Val Phe Gln Gly Glu Leu Ile
 370 375 380

Trp Gly Leu Pro Trp Asp Ile Thr Ala Tyr Gly Gly Ala Gln Phe Ser
 385 390 395 400

Glu Asp Tyr Arg Ala Leu Ala Leu Gly Leu Gly Leu Asn Leu Gly Val
 405 410 415

Phe Gly Ala Thr Ser Phe Asp Val Thr Gln Ala Asn Ser Ser Leu Val
 420 425 430

Asp Gly Ser Lys His Gln Gly Gln Ser Tyr Arg Phe Leu Tyr Ser Lys
 435 440 445

Ser Leu Val Gln Thr Gly Thr Ala Phe His Ile Ile Gly Tyr Arg Tyr
 450 455 460

Ser Thr Gln Gly Phe Tyr Thr Leu Ser Asp Thr Thr Tyr Gln Gln Met
 465 470 475 480

Ser Gly Thr Val Val Asp Pro Lys Thr Leu Asp Asp Lys Asp Tyr Val
 485 490 495

Tyr Asn Trp Asn Asp Phe Tyr Asn Leu Arg Tyr Ser Lys Arg Gly Lys
 500 505 510

Phe Gln Ala Ser Val Ser Gln Pro Phe Gly Asn Tyr Gly Ser Met Tyr
 515 520 525

Leu Ser Ala Ser Gln Gln Thr Tyr Trp Asn Thr Asp Lys Lys Asp Ser
 530 535 540

Leu Tyr Gln Val Gly Tyr Asn Thr Ser Ile Lys Gly Ile Tyr Leu Asn
 545 550 555 560

Val Ala Trp Asn Tyr Ser Lys Ser Pro Gly Thr Asn Ala Asp Lys Ile
 565 570 575

Val Ser Leu Asn Val Ser Leu Pro Ile Ser Asn Trp Leu Ser Ser Thr
 580 585 590

Asn Asp Gly Arg Ser Ser Ser Asn Ala Met Thr Ala Thr Tyr Gly Tyr
 595 600 605

Ser Gln Asp Asn His Gly Gln Val Asn Gln Tyr Thr Gly Val Ser Gly
 610 615 620

Ser Leu Leu Glu Gln His Asn Leu Ser Tyr Asn Ile Gln His Gly Phe
 625 630 635 640

Ala Asn Gln Asp Asn Ser Ser Ser Gly Ser Val Gly Val Asn Tyr Arg
 645 650 655

Gly Ala Tyr Gly Ser Leu Asn Ser Ala Tyr Ser Tyr Asp Asn Glu Gly
 660 665 670

Asn Gln Gln Ile Asn Tyr Gly Ile Ser Gly Ala Leu Val Val His Glu
 675 680 685

Asn Gly Leu Thr Leu Ser Gln Pro Leu Gly Glu Thr Asn Val Leu Ile
 690 695 700

Lys Ala Pro Gly Ala Asn Asn Val Asp Val Gln Arg Gly Thr Gly Ile
 705 710 715 720

Ser Thr Asp Trp Arg Gly Tyr Ala Val Val Pro Tyr Ala Thr Glu Tyr
 725 730 735

Arg Arg Asn Asn Ile Ser Leu Asp Pro Met Ser Met Asn Met His Thr
 740 745 750

Glu Leu Asp Ile Thr Ser Thr Glu Val Ile Pro Gly Lys Gly Ala Leu
 755 760 765

Val Arg Ala Glu Phe Ala Ala His Ile Gly Ile Arg Gly Leu Phe Thr
 770 775 780

Val Arg Tyr Arg Asn Lys Ser Val Pro Phe Gly Ala Thr Ala Ser Ala
 785 790 795 800

Gln Ile Lys Asn Ser Ser Gln Ile Thr Gly Ile Val Gly Asp Asn Gly
 805 810 815

Gln Leu Tyr Leu Ser Gly Leu Pro Leu Glu Gly Val Ile Asn Ile Gln
 820 825 830

Trp Gly Asp Gly Val Gln Gln Lys Cys Gln Ala Asn Tyr Lys Leu Pro
 835 840 845

Glu Thr Glu Leu Asp Asn Pro Val Ser Tyr Ala Thr Leu Glu Cys Arg
 850 855 860

<210> 19
 <211> 169
 <212> PRT
 <213> Escherichia coli
 <400> 19

Met Gly Ala Ile Tyr Val Lys Arg Leu Ile Leu Ser Val Ala Leu Ile
 1 5 10 15

Ile Pro Ile Ala Ser Asn Ala Ser Asp Ala Leu Asn Gln Pro Ser Ser
 20 25 30

Ser Leu Asn Asp Gly Val Glu Thr Phe Phe Ile Ser Cys Phe Asp Met
 35 40 45

Pro Gln Glu Thr Thr Thr Asp Met Asp Ala Cys Gln Arg Val Gln Leu
 50 55 60

Ala Gln Val Ser Trp Val Lys Asn Lys Tyr Ser Val Ala Ala Leu Asn
 65 70 75 80

Arg Leu Lys Gln Asp Asn Lys Asp Asp Pro Gln Arg Leu Gln Glu Leu
 85 90 95

Thr Ala Ser Phe Asn Ala Glu Ser Glu Ala Trp Thr Glu Leu Ile Glu
 100 105 110

Lys Ala Ser Lys Ser Val Gln Val Asp Tyr Val Gly Gly Thr Ile Ala
 115 120 125

Gly Thr Ala Val Ala Ser Arg Gln Ile Gly Leu Leu Glu Leu Gln Ser
 130 135 140

His Asp Ile Trp Glu His Trp Leu Arg Ser Arg Gly Leu Asn Ser Ser
 145 150 155 160

Ser Phe Ala Arg Thr Lys Val Gln Ile
165

<210> 20
<211> 713
<212> PRT
<213> Escherichia coli
<400> 20

Met Ala Met Phe Thr Pro Ser Phe Ser Gly Leu Lys Gly Arg Ala Leu
1 5 10 15

Phe Ser Leu Leu Phe Ala Ala Pro Met Ile His Ala Thr Asp Ser Val
20 25 30

Thr Thr Lys Asp Gly Glu Thr Ile Thr Val Thr Ala Asp Ala Asn Thr
35 40 45

Ala Thr Glu Ala Thr Asp Gly Tyr Gln Pro Leu Ser Thr Ser Thr Ala
50 55 60

Thr Leu Thr Asp Met Pro Met Leu Asp Ile Pro Gln Val Val Asn Thr
65 70 75 80

Val Ser Asp Gln Val Leu Glu Asn Gln Asn Ala Thr Thr Leu Asp Glu
85 90 95

Ala Leu Tyr Asn Val Ser Asn Val Val Gln Thr Asn Thr Leu Gly Gly
100 105 110

Thr Gln Asp Ala Phe Val Arg Arg Gly Phe Gly Ala Asn Arg Asp Gly
115 120 125

Ser Ile Met Thr Asn Gly Leu Arg Thr Val Leu Pro Arg Ser Phe Asn
130 135 140

Ala Ala Thr Glu Arg Val Glu Val Leu Lys Gly Pro Ala Ser Thr Leu
145 150 155 160

Tyr Gly Ile Leu Asp Pro Gly Gly Leu Ile Asn Val Val Thr Lys Arg
165 170 175

Pro Glu Lys Thr Phe His Gly Ser Val Ser Ala Thr Ser Ser Ser Phe

180

185

190

Gly Gly Gly Thr Gly Gln Leu Asp Ile Thr Gly Pro Ile Glu Gly Thr
 195 200 205

Gln Leu Ala Tyr Arg Leu Thr Gly Glu Val Gln Asp Glu Asp Tyr Trp
 210 215 220

Arg Asn Phe Gly Lys Glu Arg Ser Thr Phe Ile Ala Pro Ser Leu Thr
 225 230 235 240

Trp Phe Gly Asp Asn Ala Thr Val Thr Met Leu Tyr Ser His Arg Asp
 245 250 255

Tyr Lys Thr Pro Phe Asp Arg Gly Thr Ile Phe Asp Leu Thr Thr Lys
 260 265 270

Gln Pro Val Asn Val Asp Arg Lys Ile Arg Phe Asp Glu Pro Phe Asn
 275 280 285

Ile Thr Asp Gly Gln Ser Asp Leu Ala Gln Leu Asn Ala Glu Tyr His
 290 295 300

Leu Asn Ser Gln Trp Thr Ala Arg Phe Asp Tyr Ser Tyr Ser Gln Asp
 305 310 315 320

Lys Tyr Ser Asp Asn Gln Ala Arg Val Thr Ala Tyr Asp Ala Thr Thr
 325 330 335

Gly Thr Leu Thr Arg Arg Val Asp Ala Thr Gln Gly Ser Thr Gln Arg
 340 345 350

Met His Ala Thr Arg Ala Asp Leu Gln Gly Asn Val Asp Ile Ala Gly
 355 360 365

Phe Tyr Asn Glu Ile Leu Gly Gly Val Ser Tyr Glu Tyr Tyr Asp Leu
 370 375 380

Leu Arg Thr Asp Met Ile Arg Cys Lys Lys Ala Lys Asp Phe Asn Ile
 385 390 395 400

Tyr Asn Pro Val Tyr Gly Asn Thr Ser Lys Cys Thr Thr Val Ser Ala
 405 410 415

Ser Asp Ser Asp Gln Thr Ile Lys Gln Glu Asn Tyr Ser Ala Tyr Ala
 420 425 430

Gln Asp Ala Leu Tyr Leu Thr Asp Asn Trp Ile Ala Val Ala Gly Ile
 435 440 445

Arg Tyr Gln Tyr Tyr Thr Gln Tyr Ala Gly Lys Gly Arg Pro Phe Asn
 450 455 460

Val Asn Thr Asp Ser Arg Asp Glu Gln Trp Thr Pro Lys Leu Gly Leu
 465 470 475 480

Val Tyr Lys Leu Thr Pro Ser Val Ser Leu Phe Ala Asn Tyr Ser Gln
 485 490 495

Thr Phe Met Pro Gln Ser Ser Ile Ala Ser Tyr Ile Gly Asp Leu Pro
 500 505 510

Pro Glu Ser Ser Asn Ala Tyr Glu Val Gly Ala Lys Phe Glu Leu Phe
 515 520 525

Asp Gly Ile Thr Ala Asp Ile Ala Leu Phe Asp Ile His Lys Arg Asn
 530 535 540

Val Leu Tyr Thr Glu Ser Ile Gly Asp Glu Thr Ile Ala Lys Thr Ala
 545 550 555 560

Gly Arg Val Arg Ser Arg Gly Val Glu Val Asp Leu Ala Gly Ala Leu
 565 570 575

Thr Glu Asn Ile Asn Ile Ile Ala Ser Tyr Gly Tyr Thr Asp Ala Lys
 580 585 590

Val Leu Glu Asp Pro Asp Tyr Ala Gly Lys Pro Leu Pro Asn Val Pro
 595 600 605

Arg His Thr Gly Ser Leu Phe Leu Thr Tyr Asp Ile His Asn Met Pro
 610 615 620

Gly Asn Asn Thr Leu Thr Phe Gly Gly Gly Gly His Gly Val Ser Arg
 625 630 635 640

Arg Ser Ala Thr Asn Gly Ala Asp Tyr Tyr Leu Pro Gly Tyr Phe Val
645 650 655

Ala Asp Ala Phe Ala Ala Tyr Lys Met Lys Leu Gln Tyr Pro Val Thr
660 665 670

Leu Gln Leu Asn Val Lys Asn Leu Phe Asp Lys Thr Tyr Tyr Thr Ser
675 680 685

Ser Ile Ala Thr Asn Asn Leu Gly Asn Gln Ile Gly Asp Pro Arg Glu
690 695 700

Val Gln Phe Thr Val Lys Met Glu Phe
705 710

<210> 21
<211> 606
<212> PRT
<213> Escherichia coli
<400> 21

Met Lys Ile Ser Trp Asn Tyr Ile Phe Lys Asn Lys Trp Arg Phe His
1 5 10 15

Ile Thr Ser Ile Ser Leu Phe Leu Ile Met Leu Ala Val Ser Ile Ala
20 25 30

Phe Leu His Leu Arg Phe Asn Thr Leu Ser Ser Thr Asp Lys Met Arg
35 40 45

Leu Glu Met Tyr Lys Ser Thr Leu Tyr Ser Thr Ile Glu Gln Phe Tyr
50 55 60

Val Leu Pro Tyr Met Leu Ser Thr Asp His Ile Ile Arg Gln Ala Val
65 70 75 80

Ile Thr Pro Asp Asp Met Thr Ser Ser Glu Leu Asn Gln Arg Ile Ala
85 90 95

His Phe Asn Thr Gln Leu Lys Thr Ala Ala Ile Phe Ile Leu Asp Thr
100 105 110

Gln Gly Lys Ala Ile Ala Ser Ser Asn Trp Gln Asp Pro Gly Ser Tyr
115 120 125

Val Gly Gln Asn Tyr Ser Tyr Arg Pro Tyr Tyr Lys His Ala Met Ser
 130 135 140

Gly Leu Asn Gly Arg Phe Tyr Gly Ile Gly Ser Thr Thr Asn Thr Pro
 145 150 155 160

Gly Phe Phe Leu Ser Thr Ser Ile Lys Asp Lys Gly Lys Ile Val Gly
 165 170 175

Val Val Val Val Lys Ile Ser Leu Asn Glu Ile Glu Lys Ala Trp Ala
 180 185 190

Glu Gly Pro Glu Asn Ile Ile Val Asn Asp Glu His Gly Ile Ile Phe
 195 200 205

Leu Ser Ser Lys Ser Pro Trp Arg Met Arg Thr Leu Gln Pro Leu Pro
 210 215 220

Val Gln Ala Lys Gln Lys Leu Gln Ser Thr Arg Gln Tyr Ser Leu Asp
 225 230 235 240

Asn Leu Leu Pro Ala Asp Tyr Tyr Pro Cys Tyr Thr Val Ser Asn Phe
 245 250 255

Thr Phe Leu Lys Asp Lys Lys Glu Gln Leu Cys Leu Phe Pro Gln Tyr
 260 265 270

Tyr Thr Gln Gln Ile Ala Ile Pro Glu Phe Asn Trp Lys Met Thr Ile
 275 280 285

Met Val Pro Leu Asp Asn Leu Tyr Trp Ser Trp Ala Ile Ser Leu Val
 290 295 300

Ile Thr Leu Ile Ile Tyr Leu Leu Phe Leu Leu Phe Ile Lys Tyr Trp
 305 310 315 320

Arg Met Arg Ser His Ala Gln Gln Leu Leu Thr Leu Ala Asn Glu Thr
 325 330 335

Leu Glu Lys Gln Val Lys Glu Arg Thr Ser Ala Leu Glu Leu Ile Asn
 340 345 350

Gln Lys Leu Ile Gln Glu Ile Lys Glu Arg Ser Gln Ala Glu Gln Val
355 360 365

Leu Gln Ile Thr Arg Ser Glu Leu Ala Glu Ser Ser Lys Leu Ala Ala
370 375 380

Leu Gly Gln Met Ala Thr Glu Ile Ala His Glu Gln Asn Gln Pro Leu
385 390 395 400

Ala Ala Ile His Ala Leu Thr Asp Asn Ala Arg Thr Met Leu Lys Lys
405 410 415

Glu Met Tyr Pro Gln Val Glu Gln Asn Leu Lys His Ile Ile Ser Val
420 425 430

Ile Glu Arg Met Thr Gln Leu Ile Ser Glu Leu Lys Ala Phe Ala Ser
435 440 445

Arg His Arg Val Pro Lys Gly Ser Ala Asp Val Ile Lys Val Met Tyr
450 455 460

Ser Ala Val Ala Leu Leu Asn His Ser Met Glu Lys Asn Asn Ile Glu
465 470 475 480

Arg Arg Ile Lys Ala Pro Ser Met Pro Leu Phe Val Asn Cys Asp Glu
485 490 495

Leu Gly Leu Glu Gln Ile Phe Ser Asn Leu Ile Ser Asn Ala Leu Asp
500 505 510

Ser Met Glu Gly Ser Ser Tyr Lys Arg Leu Asp Ile Ala Ile Arg Gln
515 520 525

Ala Asn Asn Lys Val Ile Ile Thr Ile Lys Asp Ser Gly Gly Gly Phe
530 535 540

Ala Pro Glu Val Val Asp Arg Ile Phe Glu Pro Phe Phe Thr Thr Lys
545 550 555 560

Arg Arg Gly Met Gly Leu Gly Leu Ala Ile Val Ser Glu Ile Val Arg
565 570 575

46

Asn Ser Asn Gly Ala Leu His Ala Ser Asn His Pro Glu Gly Gly Ala
 580 585 590

Val Met Thr Leu Thr Trp Pro Glu Trp Gly Glu Glu His Glu
 595 600 605

<210> 22
 <211> 101
 <212> PRT
 <213> Escherichia coli
 <400> 22

Val Leu Thr Pro Gln His Leu Arg Cys Val Leu Thr Cys Ser Asp Leu
 1 5 10 15

Leu Thr Leu Leu Ser Gly Thr Val Met Ser Gln Met Pro Leu Tyr Phe
 20 25 30

Leu Asn Thr Gln Lys Lys Leu Thr Ala His Tyr Glu Trp Leu Gln Ile
 35 40 45

Asn Leu Thr Asp Thr Tyr Glu Leu Val Lys Arg Leu Met Pro Ile Pro
 50 55 60

Ser Leu Asp Val Val Val Lys Val Gly Lys Leu Val Leu Pro Glu Lys
 65 70 75 80

Gly His His Gly Phe Tyr Pro Glu Ala Gly Val Val Tyr Arg Thr Val
 85 90 95

Ala Pro Glu Asn Pro
 100

<210> 23
 <211> 263
 <212> PRT
 <213> Escherichia coli
 <400> 23

Met Met Lys Asn Thr Gly Tyr Ile Leu Ala Leu Cys Leu Thr Ala Ser
 1 5 10 15

Gly His Val Leu Ala His Asp Val Trp Ile Thr Gly Lys Gln Ala Glu
 20 25 30

Asn Asn Val Thr Ala Glu Ile Gly Tyr Gly His Asn Phe Pro Ser Lys

35 40 45

Gly Thr Ile Pro Asp Arg Arg Asp Phe Phe Glu Asn Pro Arg Leu Tyr
50 55 60

Asn Gly Lys Glu Thr Ile Thr Leu Lys Pro Ala Ser Thr Asp Tyr Val
65 70 75 80

Tyr Lys Thr Glu Ser Ala Ser Lys Asp Asn Gly Tyr Val Leu Ser Thr
85 90 95

Tyr Met Lys Pro Gly Tyr Trp Ser Arg Thr Ser Ser Gly Trp Lys Pro
100 105 110

Val Ser Arg Glu Gly Arg Asn Asp Val Ala Tyr Cys Glu Phe Val Thr
115 120 125

Lys Tyr Ala Lys Ser Phe Ile Pro Gly Glu Gln Gln Met Pro Ala Gln
130 135 140

Leu Tyr Gln Ser Pro Thr Gly His Glu Leu Glu Ile Ile Pro Leu Ser
145 150 155 160

Asp Ile Ser Arg Phe Ser Glu Asn Val Lys Leu Lys Val Leu Tyr Lys
165 170 175

Thr Ser Pro Leu Ala Gly Ala Ile Met Glu Leu Asp Ser Val Ser Tyr
180 185 190

Leu Thr Ser Ser Arg His Thr His Ala Val Glu His Lys His Pro Val
195 200 205

His Lys Ala Glu Leu Thr Phe Val Thr Asn Glu Asp Gly Ile Val Thr
210 215 220

Val Pro Ser Leu His Ile Gly Gln Trp Leu Ala Lys Val Gln Asn Lys
225 230 235 240

Lys Ser Phe Gln Asp Lys Ser Leu Cys Asp Glu Thr Val Asp Val Ala
245 250 255

Thr Leu Ser Phe Ser Arg Asn
260

<210> 24
 <211> 378
 <212> PRT
 <213> Escherichia coli
 <400> 24

Met Gly Lys Ile Lys Tyr Trp Leu Ile Val Gly Phe Ile Ile Leu Phe
 1 5 10 15

Ala Ile Phe Tyr Ile Ala Ile Ser Asp Arg Asp Ser Thr Leu Ser Arg
 20 25 30

Leu Lys Ser Ala Gly Glu Asn Gly Asp Val Glu Ala Gln Tyr Ala Leu
 35 40 45

Gly Leu Met Tyr Leu Tyr Gly Glu Ile Leu Asp Val Asp Tyr Gln Gln
 50 55 60

Ala Lys Ile Trp Tyr Glu Lys Ala Ala Asp Gln Asn Asp Pro Arg Ala
 65 70 75 80

Gln Ala Lys Leu Gly Val Met Tyr Ala Asn Gly Leu Gly Val Asn Gln
 85 90 95

Asp Tyr Gln Gln Ser Lys Leu Trp Tyr Glu Lys Ala Ala Ala Gln Asn
 100 105 110

Asp Val Asp Ala Gln Phe Leu Leu Gly Glu Met Tyr Asp Asp Gly Leu
 115 120 125

Gly Val Ser Gln Asp Tyr Gln His Ala Lys Met Trp Tyr Glu Lys Ala
 130 135 140

Ala Ala Gln Asn Asp Glu Arg Ala Gln Val Asn Leu Ala Val Leu Tyr
 145 150 155 160

Ala Lys Gly Asn Gly Val Glu Gln Asp Tyr Arg Gln Ala Lys Ser Trp
 165 170 175

Tyr Glu Lys Ala Ala Ala Gln Asn Ser Pro Asp Ala Gln Phe Ala Leu
 180 185 190

Gly Ile Leu Tyr Ala Asn Ala Asn Gly Val Glu Gln Asp Tyr Gln Gln

195	200	205
Ala Lys Asp Trp Tyr Glu Lys Ala Ala Glu Gln Asn Phe Ala Asn Ala		
210	215	220
Gln Phe Asn Leu Gly Met Leu Tyr Tyr Lys Gly Glu Gly Val Lys Gln		
225	230	235 240
Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn		
245	250	255
Gln Pro Asn Ala Gln Tyr Asn Leu Gly Gln Ile Tyr Tyr Tyr Gly Gln		
260	265	270
Gly Val Thr Gln Ser Tyr Arg Gln Ala Lys Asp Trp Phe Glu Lys Ala		
275	280	285
Ala Glu Lys Gly His Val Asp Ala Gln Tyr Asn Leu Gly Val Ile Tyr		
290	295	300
Glu Asn Gly Glu Gly Val Ser Gln Asn Tyr Gln Gln Ala Lys Ala Trp		
305	310	315 320
Tyr Glu Lys Ala Ala Ser Gln Asn Asp Ala Gln Ala Gln Phe Glu Leu		
325	330	335
Gly Val Met Asn Glu Leu Gly Gln Gly Glu Ser Ile Asp Leu Lys Gln		
340	345	350
Ala Arg His Tyr Tyr Glu Arg Ser Cys Asn Asn Gly Leu Lys Lys Gly		
355	360	365
Cys Glu Arg Leu Lys Glu Leu Leu Tyr Lys		
370	375	

<210> 25
 <211> 654
 <212> PRT
 <213> Escherichia coli
 <400> 25

Met Asn Val Ile Arg Thr Val Ile Cys Thr Leu Ile Ile Leu Pro Val
1 5 10 15

50

Gly Leu Gln Ala Ala Thr Ser His Ser Ser Met Val Lys Asp Thr Ile
 20 25 30

Thr Ile Val Ala Thr Gly Asn Gln Asn Thr Val Phe Glu Thr Pro Ser
 35 40 45

Met Val Ser Val Val Thr Asn Asp Thr Pro Trp Ser Gln Asn Ala Val
 50 55 60

Thr Ser Ala Gly Met Leu Lys Gly Val Ala Gly Leu Ser Gln Thr Gly
 65 70 75 80

Ala Gly Arg Thr Asn Gly Gln Thr Phe Asn Leu Arg Gly Tyr Asp Lys
 85 90 95

Ser Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Leu Ser Asp Met
 100 105 110

Ala Lys Ser Ser Gly Thr Tyr Leu Asp Pro Ala Leu Val Lys Arg Ile
 115 120 125

Glu Val Val Arg Gly Pro Asn Ser Ser Leu Tyr Gly Ser Gly Gly Leu
 130 135 140

Gly Gly Val Val Asp Phe Arg Thr Ala Asp Ala Ala Asp Phe Leu Pro
 145 150 155 160

Pro Gly Glu Thr Asn Gly Leu Ser Leu Trp Gly Asn Ile Ala Ser Gly
 165 170 175

Asp His Ser Thr Gly Ser Gly Leu Thr Trp Phe Gly Lys Thr Gly Lys
 180 185 190

Thr Asp Ala Leu Leu Ser Val Ile Met Arg Lys Arg Gly Asn Ile Tyr
 195 200 205

Gln Ser Asp Gly Glu His Ala Pro Asn Lys Glu Lys Pro Ala Ala Leu
 210 215 220

Phe Ala Lys Gly Ser Val Gly Ile Thr Asp Ser Asn Lys Ala Gly Ala
 225 230 235 240

Ser Leu Arg Leu Tyr Arg Asn Asn Thr Thr Glu Pro Gly Asn Ser Thr

Asn Ile Thr Arg Glu Ile Gly Ala Gly Ile Gln Leu Asp Gly Leu Leu
465 470 475 480

Thr Asp Asn Asp Arg Leu Gln Leu Lys Gly Gly Tyr Phe Gly Thr Asp
 485 490 495

Ala Arg Asn Tyr Ile Ala Thr Arg Val Asp Met Lys Arg Met Arg Ser
 500 505 510

Tyr Ser Tyr Asn Val Ser Arg Ala Arg Ile Trp Gly Trp Asp Met Gln
 515 520 525

Gly Asn Tyr Gln Ser Asp Tyr Val Asp Trp Met Leu Ser Tyr Asn Arg
 530 535 540

Thr Glu Ser Met Asp Ala Ser Ser Arg Glu Trp Leu Gly Ser Gly Asn
 545 550 555 560

Pro Asp Thr Leu Ile Ser Asp Ile Ser Ile Pro Val Gly His Arg Gly
 565 570 575

Val Tyr Ala Gly Trp Arg Ala Glu Leu Ser Ala Ser Ala Thr His Val
 580 585 590

Lys Lys Gly Asp Pro His Gln Ala Gly Tyr Thr Ile His Ser Phe Ser
 595 600 605

Leu Ser Tyr Lys Pro Val Ser Val Lys Gly Phe Glu Ala Ser Val Thr
 610 615 620

Leu Asp Asn Ala Phe Asn Lys Leu Ala Met Asn Gly Lys Gly Val Pro
 625 630 635 640

Leu Ser Gly Arg Thr Val Ser Leu Tyr Thr Arg Tyr Gln Trp
 645 650

<210> 26
 <211> 1376
 <212> PRT
 <213> Escherichia coli
 <400> 26

Met Asn Lys Ile Tyr Ala Leu Lys Tyr Cys Tyr Ile Thr Asn Thr Val
 1 5 10 15

Lys Val Val Ser Glu Leu Ala Arg Arg Val Cys Lys Gly Ser Thr Arg

20 25 30
 Arg Gly Lys Arg Leu Ser Val Leu Thr Ser Leu Ala Leu Ser Ala Leu
 35 40 45
 Leu Pro Thr Val Ala Gly Ala Ser Thr Val Gly Gly Asn Asn Pro Tyr
 50 55 60
 Gln Thr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Gln Phe Gln Ala Gly
 65 70 75 80
 Ala Thr Asn Ile Pro Ile Phe Asn Asn Lys Gly Glu Leu Val Gly His
 85 90 95
 Leu Asp Lys Ala Pro Met Val Asp Phe Ser Ser Val Asn Val Ser Ser
 100 105 110
 Asn Pro Gly Val Ala Thr Leu Ile Asn Pro Gln Tyr Ile Ala Ser Val
 115 120 125
 Lys His Asn Lys Gly Tyr Gln Ser Val Ser Phe Gly Asp Gly Gln Asn
 130 135 140
 Ser Tyr His Ile Val Asp Arg Asn Glu His Ser Ser Ser Asp Leu His
 145 150 155 160
 Thr Pro Arg Leu Asp Lys Leu Val Thr Glu Val Ala Pro Ala Thr Val
 165 170 175
 Thr Ser Ser Ser Thr Ala Asp Ile Leu Asn Pro Ser Lys Tyr Ser Ala
 180 185 190
 Phe Tyr Arg Ala Gly Ser Gly Ser Gln Tyr Ile Gln Asp Ser Gln Gly
 195 200 205
 Lys Arg His Trp Val Thr Gly Gly Tyr Gly Tyr Leu Thr Gly Gly Ile
 210 215 220
 Leu Pro Thr Ser Phe Phe Tyr His Gly Ser Asp Gly Ile Gln Leu Tyr
 225 230 235 240
 Met Gly Gly Asn Ile His Asp His Ser Ile Leu Pro Ser Phe Gly Glu
 245 250 255

Ala Gly Asp Ser Gly Ser Pro Leu Phe Gly Trp Asn Thr Ala Lys Gly
 260 265 270

Gln Trp Glu Leu Val Gly Val Tyr Ser Gly Val Gly Gly Gly Thr Asn
 275 280 285

Leu Ile Tyr Ser Leu Ile Pro Gln Ser Phe Leu Ser Gln Ile Tyr Ser
 290 295 300

Glu Asp Asn Asp Ala Pro Val Phe Phe Asn Ala Ser Ser Gly Ala Pro
 305 310 315 320

Leu Gln Trp Lys Phe Asp Ser Ser Thr Gly Thr Gly Ser Leu Lys Gln
 325 330 335

Gly Ser Asp Glu Tyr Ala Met His Gly Gln Lys Gly Ser Asp Leu Asn
 340 345 350

Ala Gly Lys Asn Leu Thr Phe Leu Gly His Asn Gly Gln Ile Asp Leu
 355 360 365

Glu Asn Ser Val Thr Gln Gly Ala Gly Ser Leu Thr Phe Thr Asp Asp
 370 375 380

Tyr Thr Val Thr Thr Ser Asn Gly Ser Thr Trp Thr Gly Ala Gly Ile
 385 390 395 400

Ile Val Asp Lys Asp Ala Ser Val Asn Trp Gln Val Asn Gly Val Lys
 405 410 415

Gly Asp Asn Leu His Lys Ile Gly Glu Gly Thr Leu Val Val Gln Gly
 420 425 430

Thr Gly Val Asn Glu Gly Gly Leu Lys Val Gly Asp Gly Thr Val Val
 435 440 445

Leu Asn Gln Gln Ala Asp Ser Ser Gly His Val Gln Ala Phe Ser Ser
 450 455 460

Val Asn Ile Ala Ser Gly Arg Pro Thr Val Val Leu Ala Asp Asn Gln
 465 470 475 480

Gln Val Asn Pro Asp Asn Ile Ser Trp Gly Tyr Arg Gly Gly Val Leu
 485 490 495

Asp Val Asn Gly Asn Asp Leu Thr Phe His Lys Leu Asn Ala Ala Asp
 500 505 510

Tyr Gly Ala Thr Leu Gly Asn Ser Ser Asp Lys Thr Ala Asn Ile Thr
 515 520 525

Leu Asp Tyr Gln Thr Arg Pro Ala Asp Val Lys Val Asn Glu Trp Ser
 530 535 540

Ser Ser Asn Arg Gly Thr Val Gly Ser Leu Tyr Ile Tyr Asn Asn Pro
 545 550 555 560

Tyr Thr His Thr Val Asp Tyr Phe Ile Leu Lys Thr Ser Ser Tyr Gly
 565 570 575

Trp Phe Pro Thr Gly Gln Val Ser Asn Glu His Trp Glu Tyr Val Gly
 580 585 590

His Asp Gln Asn Ser Ala Gln Ala Leu Leu Ala Asn Arg Ile Asn Asn
 595 600 605

Lys Gly Tyr Leu Tyr His Gly Lys Leu Leu Gly Asn Ile Asn Phe Ser
 610 615 620

Asn Lys Ala Thr Pro Gly Thr Thr Gly Ala Leu Val Met Asp Gly Ser
 625 630 635 640

Ala Asn Met Ser Gly Thr Phe Thr Gln Glu Asn Gly Arg Leu Thr Ile
 645 650 655

Gln Gly His Pro Val Ile His Ala Ser Thr Ser Gln Ser Ile Ala Asn
 660 665 670

Thr Val Ser Ser Leu Gly Asp Asn Ser Val Leu Thr Gln Pro Thr Ser
 675 680 685

Phe Thr Gln Asp Asp Trp Glu Asn Arg Thr Phe Ser Phe Gly Ser Leu
 690 695 700

56

Val Leu Lys Asp Thr Asp Phe Gly Leu Gly Arg Asn Ala Thr Leu Asn
705 710 715 720

Thr Thr Ile Gln Ala Asp Asn Ser Ser Val Thr Leu Gly Asp Ser Arg
725 730 735

Val Phe Ile Asp Lys Lys Asp Gly Gln Gly Thr Ala Phe Thr Leu Glu
740 745 750

Glu Gly Thr Ser Val Ala Thr Lys Asp Ala Asp Lys Ser Val Phe Asn
755 760 765

Gly Thr Val Asn Leu Asp Asn Gln Ser Val Leu Asn Ile Asn Glu Ile
770 775 780

Phe Asn Gly Gly Ile Gln Ala Asn Asn Ser Thr Val Asn Ile Ser Ser
785 790 795 800

Asp Ser Ala Val Leu Glu Asn Ser Thr Leu Thr Ser Thr Ala Leu Asn
805 810 815

Leu Asn Lys Gly Ala Asn Val Leu Ala Ser Gln Ser Phe Val Ser Asp
820 825 830

Gly Pro Val Asn Ile Ser Asp Ala Thr Leu Ser Leu Asn Ser Arg Pro
835 840 845

Asp Glu Val Ser His Thr Leu Leu Pro Val Tyr Asp Tyr Ala Gly Ser
850 855 860

Trp Asn Leu Lys Gly Asp Asp Ala Arg Leu Asn Val Gly Pro Tyr Ser
865 870 875 880

Met Leu Ser Gly Asn Ile Asn Val Gln Asp Lys Gly Thr Val Thr Leu
885 890 895

Gly Gly Glu Gly Glu Leu Ser Pro Asp Leu Thr Leu Gln Asn Gln Met
900 905 910

Leu Tyr Ser Leu Phe Asn Gly Tyr Arg Asn Thr Trp Ser Gly Ser Leu
915 920 925

Asn Ala Pro Asp Ala Thr Val Ser Met Thr Asp Thr Gln Trp Ser Met

930

935

940

Asn Gly Asn Ser Thr Ala Gly Asn Met Lys Leu Asn Arg Thr Ile Val
 945 950 955 960

Gly Phe Asn Gly Gly Thr Ser Ser Phe Thr Thr Leu Thr Thr Asp Asn
 965 970 975

Leu Asp Ala Val Gln Ser Ala Phe Val Met Arg Thr Asp Leu Asn Lys
 980 985 990

Ala Asp Lys Leu Val Ile Asn Lys Ser Ala Thr Gly His Asp Asn Ser
 995 1000 1005

Ile Trp Val Asn Phe Leu Lys Lys Pro Ser Asp Lys Asp Thr Leu
 1010 1015 1020

Asp Ile Pro Leu Val Ser Ala Pro Glu Ala Thr Ala Asp Asn Leu
 1025 1030 1035

Phe Arg Ala Ser Thr Arg Val Val Gly Phe Ser Asp Val Thr Pro
 1040 1045 1050

Thr Leu Ser Val Arg Lys Glu Asp Gly Lys Lys Glu Trp Val Leu
 1055 1060 1065

Asp Gly Tyr Gln Val Ala Arg Asn Asp Gly Gln Gly Lys Ala Ala
 1070 1075 1080

Ala Thr Phe Met His Ile Ser Tyr Asn Asn Phe Ile Thr Glu Val
 1085 1090 1095

Asn Asn Leu Asn Lys Arg Met Gly Asp Leu Arg Asp Ile Asn Gly
 1100 1105 1110

Glu Ala Gly Thr Trp Val Arg Leu Leu Asn Gly Ser Gly Ser Ala
 1115 1120 1125

Asp Gly Gly Phe Thr Asp His Tyr Thr Leu Leu Gln Met Gly Ala
 1130 1135 1140

Asp Arg Lys His Glu Leu Gly Ser Met Asp Leu Phe Thr Gly Val
 1145 1150 1155

Met Ala Thr Tyr Thr Asp Thr Asp Ala Ser Ala Gly Leu Tyr Ser
 1160 1165 1170

Gly Lys Thr Lys Ser Trp Gly Gly Gly Phe Tyr Ala Ser Gly Leu
 1175 1180 1185

Phe Arg Ser Gly Ala Tyr Phe Asp Leu Ile Ala Lys Tyr Ile His
 1190 1195 1200

Asn Glu Asn Lys Tyr Asp Leu Asn Phe Ala Gly Ala Gly Lys Gln
 1205 1210 1215

Asn Phe Arg Ser His Ser Leu Tyr Ala Gly Ala Glu Val Gly Tyr
 1220 1225 1230

Arg Tyr His Leu Thr Asp Thr Thr Phe Val Glu Pro Gln Ala Glu
 1235 1240 1245

Leu Val Trp Gly Arg Leu Gln Gly Gln Thr Phe Asn Trp Asn Asp
 1250 1255 1260

Ser Gly Met Asp Val Ser Met Arg Arg Asn Ser Val Asn Pro Leu
 1265 1270 1275

Val Gly Arg Thr Gly Val Val Ser Gly Lys Thr Phe Ser Gly Lys
 1280 1285 1290

Asp Trp Ser Leu Thr Ala Arg Ala Gly Leu His Tyr Glu Phe Asp
 1295 1300 1305

Leu Thr Asp Ser Ala Asp Val His Leu Lys Asp Ala Ala Gly Glu
 1310 1315 1320

His Gln Ile Asn Gly Arg Lys Asp Gly Arg Met Leu Tyr Gly Val
 1325 1330 1335

Gly Leu Asn Ala Arg Phe Gly Asp Asn Thr Arg Leu Gly Leu Glu
 1340 1345 1350

Val Glu Arg Ser Ala Phe Gly Lys Tyr Asn Thr Asp Asp Ala Ile
 1355 1360 1365

Asn Ala Asn Ile Arg Tyr Ser Phe
1370 1375

<210> 27
<211> 349
<212> PRT
<213> Escherichia coli
<400> 27

Met Ile Thr Leu Phe Arg Leu Leu Ala Ile Leu Cys Leu Phe Phe Asn
1 5 10 15

Val Ser Ala Phe Ala Val Asp Cys Tyr Gln Asp Gly Tyr Arg Gly Thr
20 25 30

Thr Leu Ile Asn Gly Asp Leu Pro Thr Phe Lys Ile Pro Glu Asn Ala
35 40 45

Gln Pro Gly Gln Lys Ile Trp Glu Ser Gly Asp Ile Asn Ile Thr Val
50 55 60

Tyr Cys Asp Asn Ala Pro Gly Trp Ser Ser Asn Asn Pro Ser Glu Asn
65 70 75 80

Val Tyr Ala Trp Ile Lys Leu Pro Gln Ile Asn Ser Ala Asp Met Leu
85 90 95

Asn Asn Pro Tyr Leu Thr Phe Gly Val Thr Tyr Asn Gly Val Asp Tyr
100 105 110

Glu Gly Thr Asn Glu Lys Ile Asp Thr His Ala Cys Leu Asp Lys Tyr
115 120 125

Glu Gln Tyr Tyr Asn Gly Tyr Tyr His Asp Pro Val Cys Asn Gly Ser
130 135 140

Thr Leu Gln Lys Asn Val Thr Phe Asn Ala His Phe Arg Val Tyr Val
145 150 155 160

Lys Phe Lys Ser Arg Pro Ala Gly Asp Gln Thr Val Asn Phe Gly Thr
165 170 175

Val Asn Val Leu Gln Phe Asp Gly Glu Gly Gly Ala Asn Met Ala Pro
180 185 190

Asn Ala Lys Asn Leu Arg Tyr Ala Ile Thr Gly Leu Asp Asn Ile Ser
 195 200 205

Phe Leu Asp Cys Ser Val Asp Val Arg Ile Ser Pro Glu Ser Gln Ile
 210 215 220

Val Asn Phe Gly Gln Ile Ala Ala Asn Ser Ile Ala Thr Phe Pro Pro
 225 230 235 240

Lys Ala Ala Phe Ser Val Ser Thr Ile Lys Asp Ile Ala Ser Asp Cys
 245 250 255

Thr Glu Gln Phe Asp Val Ala Thr Ser Phe Phe Thr Ser Asp Thr Leu
 260 265 270

Tyr Asp Asn Thr His Leu Glu Ile Gly Asn Gly Leu Leu Met Arg Ile
 275 280 285

Thr Asp Gln Lys Thr Gln Glu Asp Ile Lys Phe Asn Gln Phe Lys Leu
 290 295 300

Phe Ser Thr Tyr Ile Pro Gly Gln Ser Ala Ala Met Ala Thr Arg Asp
 305 310 315 320

Tyr Gln Ala Glu Leu Thr Gln Lys Pro Gly Glu Pro Leu Val Tyr Gly
 325 330 335

Pro Phe Gln Lys Asp Leu Ile Val Lys Ile Asn Tyr His
 340 345

<210> 28

<211> 840

<212> PRT

<213> Escherichia coli

<400> 28

Met Asn Asn Lys Asn Thr Phe Ser Arg Asp Lys Leu Ser His Ala Ile
 1 5 10 15

Lys Asn Ala Leu Ser Gly Val Val Cys Ser Leu Leu Phe Val Leu Pro
 20 25 30

Val His Ala Val Glu Phe Asn Val Asp Met Ile Asp Ala Glu Asp Arg

61

35

40

45

Glu Asn Ile Asp Ile Ser Arg Phe Glu Lys Lys Gly Tyr Ile Pro Pro
 50 55 60

Gly Arg Tyr Leu Val Arg Val Gln Ile Asn Lys Asn Met Leu Pro Gln
 65 70 75 80

Thr Leu Ile Leu Glu Trp Val Lys Ala Asp Asn Glu Ser Gly Ser Leu
 85 90 95

Leu Cys Leu Thr Lys Glu Asn Leu Thr Asn Phe Gly Leu Asn Thr Glu
 100 105 110

Phe Ile Glu Ser Leu Gln Asn Ile Ala Gly Ser Glu Cys Leu Asp Leu
 115 120 125

Ser Gln Arg Gln Glu Leu Thr Thr Arg Leu Asp Lys Ala Thr Met Ile
 130 135 140

Leu Ser Leu Ser Val Pro Gln Ala Trp Leu Lys Tyr Gln Ala Thr Asn
 145 150 155 160

Trp Thr Pro Pro Glu Phe Trp Asp Thr Gly Ile Thr Gly Phe Ile Leu
 165 170 175

Asp Tyr Asn Val Tyr Ala Ser Gln Tyr Ala Pro His His Gly Asp Ser
 180 185 190

Thr Gln Asn Val Ser Ser Tyr Gly Thr Leu Gly Phe Asn Leu Gly Ala
 195 200 205

Trp Arg Leu Arg Ser Asp Tyr Gln Tyr Asn Gln Asn Phe Ala Asp Gly
 210 215 220

Arg Ser Val Asn Arg Asp Ser Glu Phe Ala Arg Thr Tyr Leu Phe Arg
 225 230 235 240

Pro Ile Pro Ser Trp Ser Ser Lys Phe Thr Met Gly Gln Tyr Asp Leu
 245 250 255

Ser Ser Asn Leu Tyr Asp Thr Phe His Phe Thr Gly Ala Ser Leu Glu
 260 265 270

Ser Asp Glu Ser Met Leu Pro Pro Asp Leu Gln Gly Tyr Ala Pro Gln
275 280 285

Ile Thr Gly Ile Ala Gln Thr Asn Ala Lys Val Thr Val Ala Gln Asn
290 295 300

Gly Arg Val Leu Tyr Gln Thr Thr Val Ala Pro Gly Pro Phe Thr Ile
305 310 315 320

Ser Asp Leu Gly Gln Ser Phe Gln Gly Gln Leu Asp Val Thr Val Glu
325 330 335

Glu Glu Asp Gly Arg Thr Ser Thr Phe Gln Val Gly Ser Ala Ser Ile
340 345 350

Pro Tyr Leu Thr Arg Lys Gly Gln Val Arg Tyr Lys Thr Ser Leu Gly
355 360 365

Lys Pro Thr Ser Val Gly His Asn Asp Ile Asn Asn Pro Phe Phe Trp
370 375 380

Thr Ala Glu Ala Ser Trp Gly Trp Leu Asn Asn Val Ser Leu Tyr Gly
385 390 395 400

Gly Gly Met Phe Thr Ala Asp Asp Tyr Gln Ala Ile Thr Thr Gly Ile
405 410 415

Gly Phe Asn Leu Asn Gln Phe Gly Ser Leu Ser Phe Asp Val Thr Gly
420 425 430

Ala Asp Ala Ser Leu Gln Gln Gln Asn Ser Gly Asn Leu Arg Gly Tyr
435 440 445

Ser Tyr Arg Phe Asn Tyr Ala Lys His Phe Glu Ser Thr Gly Ser Gln
450 455 460

Ile Thr Phe Ala Gly Tyr Arg Phe Ser Asp Lys Asp Tyr Val Ser Met
465 470 475 480

Ser Glu Tyr Leu Ser Ser Arg Asn Gly Asp Glu Ser Ile Asp Asn Glu
485 490 495

Lys Glu Ser Tyr Val Ile Ser Leu Asn Gln Tyr Phe Glu Thr Leu Glu
 500 505 510

Leu Asn Ser Tyr Leu Asn Val Thr Arg Asn Thr Tyr Trp Asp Ser Ala
 515 520 525

Ser Asn Thr Asn Tyr Ser Val Ser Val Ser Lys Asn Phe Asp Ile Gly
 530 535 540

Asp Phe Lys Gly Ile Ser Ala Ser Leu Ala Val Ser Arg Ile Arg Trp
 545 550 555 560

Asp Asp Asp Glu Glu Asn Gln Tyr Tyr Phe Ser Phe Ser Leu Pro Leu
 565 570 575

Gln Gln Asn Arg Asn Ile Ser Tyr Ser Met Gln Arg Thr Gly Ser Ser
 580 585 590

Asn Thr Ser Gln Met Ile Ser Trp Tyr Asp Ser Ser Asp Arg Asn Asn
 595 600 605

Ile Trp Asn Ile Ser Ala Ser Ala Thr Asp Asp Asn Ile Arg Asp Gly
 610 615 620

Glu Pro Thr Leu Arg Gly Ser Tyr Gln His Tyr Ser Pro Trp Gly Arg
 625 630 635 640

Leu Asn Ile Asn Gly Ser Val Gln Pro Asn Gln Tyr Asn Ser Val Thr
 645 650 655

Ala Gly Trp Tyr Gly Ser Leu Thr Ala Thr Arg His Gly Val Ala Leu
 660 665 670

His Asp Tyr Ser Tyr Gly Asp Asn Ala Arg Met Met Val Asp Thr Asp
 675 680 685

Gly Ile Ser Gly Ile Glu Ile Asn Ser Asn Arg Thr Val Thr Asn Gly
 690 695 700

Leu Gly Ile Ala Val Ile Pro Ser Leu Ser Asn Tyr Thr Thr Ser Met
 705 710 715 720

Leu Arg Val Asn Asn Asn Asp Leu Pro Glu Gly Val Asp Val Glu Asn
 725 730 735

Ser Val Ile Arg Thr Thr Leu Thr Gln Gly Ala Ile Gly Tyr Ala Lys
 740 745 750

Leu Asn Ala Thr Thr Gly Tyr Gln Ile Val Gly Val Ile Arg Gln Glu
 755 760 765

Asn Gly Arg Phe Pro Pro Leu Gly Val Asn Val Thr Asp Lys Ala Thr
 770 775 780

Gly Lys Asp Val Gly Leu Val Ala Glu Asp Gly Phe Val Tyr Leu Ser
 785 790 795 800

Gly Ile Gln Glu Asn Ser Ile Leu His Leu Thr Trp Gly Asp Asn Thr
 805 810 815

Cys Glu Val Thr Pro Pro Asn Gln Ser Asn Ile Ser Glu Ser Ala Ile
 820 825 830

Ile Leu Pro Cys Lys Thr Val Lys
 835 840

<210> 29
 <211> 169
 <212> PRT
 <213> Escherichia coli
 <400> 29

Leu Met Asn Thr Lys Gln Ser Val Ala Gln Leu Ala Val Pro His Arg
 1 5 10 15

Lys Arg Leu Ser Ser Thr Met Val Val Ala Leu Leu Leu Cys Val Val
 20 25 30

Ala Gly Ala Val Met Ile Asn Ala Ala Asp Phe Pro Ala Thr Ala Ile
 35 40 45

Glu Thr Asp Pro Gly Ala Ser Ala Phe Pro Thr Phe Tyr Ala Cys Ala
 50 55 60

Leu Ile Val Leu Ala Val Leu Leu Val Ile Arg Asp Leu Leu Gln Ala
 65 70 75 80

Met Val Arg Phe Lys Thr Ser Asp Phe Lys Pro Ile Ala Arg Leu Asn
100 105 110

Ala Asp Pro Ala Ala Ile Thr Val Arg Ala Asp Ala Pro Trp Asn Ser
 115 120 125

Tyr Glu Glu Phe Met Ala Tyr Ser Lys Ala Asn Pro Gly Lys Val Arg
 130 135 140

Ile Gly Asn Ser Gly Thr Gly Ala Ile Trp His Leu Ala Ala Ala Ala
 145 150 155 160

Leu Glu Asp Lys Thr Gly Thr Lys Phe Ser His Val Pro Tyr Asp Gly
 165 170 175

Ala Ala Pro Ala Ile Thr Gly Leu Leu Gly Gly His Ile Glu Ala Val
 180 185 190

Ser Val Ser Pro Gly Glu Val Ile Asn His Val Asn Gly Gly Lys Leu
 195 200 205

Lys Thr Leu Val Val Met Ala Asp Glu Arg Met Lys Thr Met Pro Asp
 210 215 220

Val Pro Thr Leu Lys Glu Lys Gly Val Asp Leu Ser Ile Gly Thr Trp
 225 230 235 240

Arg Gly Leu Ile Val Ser Gln Lys Thr Pro Gln Asp Val Val Asp Val
 245 250 255

Leu Ala Lys Ala Ala Lys Glu Thr Ala Glu Glu Pro Ala Phe Gln Asp
 260 265 270

Ala Leu Gln Lys Leu Asn Leu Asn Tyr Ala Trp Leu Asp Ala Ala Ser
 275 280 285

Phe Gln Thr Gln Ile Ser Glu Gln Glu Lys Tyr Phe Asp Glu Leu Leu
 290 295 300

Thr Arg Leu Gly Leu Lys Lys
 305 310

<210> 31
 <211> 722
 <212> PRT

<213> Escherichia coli
<400> 31

Met Leu Arg Trp Lys Arg Cys Ile Ile Leu Thr Phe Ile Ser Gly Ala
1 5 10 15

Ala Phe Ala Ala Pro Glu Ile Asn Val Lys Gln Asn Glu Ser Leu Pro
20 25 30

Asp Leu Gly Ser Gln Ala Ala Gln Gln Asp Glu Gln Thr Asn Lys Gly
35 40 45

Lys Ser Leu Lys Glu Arg Gly Ala Asp Tyr Val Ile Asn Ser Ala Thr
50 55 60

Gln Gly Phe Glu Asn Leu Thr Pro Glu Ala Leu Glu Ser Gln Ala Arg
65 70 75 80

Ser Tyr Leu Gln Ser Gln Ile Thr Ser Thr Ala Gln Ser Tyr Ile Glu
85 90 95

Asp Thr Leu Ser Pro Tyr Gly Lys Val Arg Leu Asn Leu Ser Ile Gly
100 105 110

Gln Gly Gly Asp Leu Asp Gly Ser Ser Ile Asp Tyr Phe Val Pro Trp
115 120 125

Tyr Asp Asn Gln Thr Thr Val Tyr Phe Ser Gln Phe Ser Ala Gln Arg
130 135 140

Lys Glu Asp Arg Thr Ile Gly Asn Ile Gly Leu Gly Val Arg Tyr Asn
145 150 155 160

Phe Asp Lys Tyr Leu Leu Gly Gly Asn Ile Phe Tyr Asp Tyr Asp Phe
165 170 175

Thr Arg Gly His Arg Arg Leu Gly Leu Gly Ala Glu Ala Trp Thr Asp
180 185 190

Tyr Leu Lys Phe Ser Gly Asn Tyr Tyr His Pro Leu Ser Asp Trp Lys
195 200 205

Asp Ser Glu Asp Phe Asp Phe Tyr Glu Glu Arg Pro Ala Arg Gly Trp
210 215 220

Asp Ile Arg Ala Glu Val Trp Leu Pro Ser Tyr Pro Gln Leu Gly Gly
225 230 235 240

Lys Ile Val Phe Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Gly
245 250 255

Thr Asp Asn Leu Glu Lys Asp Pro Tyr Ala Val Thr Leu Gly Leu Asn
260 265 270

Tyr Gln Pro Val Pro Leu Leu Thr Val Gly Thr Asp Tyr Lys Ala Gly
275 280 285

Thr Gly Asp Asn Ser Asp Val Ser Ile Asn Ala Thr Leu Asn Tyr Gln
290 295 300

Phe Gly Val Pro Leu Lys Asp Gln Leu Asp Ser Asp Lys Val Lys Ala
305 310 315 320

Ala His Ser Leu Met Gly Ser Arg Leu Asp Phe Val Glu Arg Asn Asn
325 330 335

Phe Ile Val Leu Glu Tyr Lys Glu Lys Asp Pro Leu Asp Val Thr Leu
340 345 350

Trp Leu Lys Ala Asp Ala Thr Asn Glu His Pro Glu Cys Val Ile Lys
355 360 365

Asp Thr Pro Glu Ala Ala Val Gly Leu Glu Lys Cys Lys Trp Thr Ile
370 375 380

Asn Ala Leu Ile Asn His His Tyr Lys Ile Val Ala Ala Ser Trp Gln
385 390 395 400

Ala Lys Asn Asn Ala Ala Arg Thr Leu Val Met Pro Val Ile Lys Glu
405 410 415

Asn Thr Leu Thr Glu Gly Asn Asn Asn His Trp Asn Leu Val Leu Pro
420 425 430

Ala Trp Gln Tyr Ser Ser Asp Gln Ala Glu Gln Glu Lys Leu Asn Thr
435 440 445

Trp Arg Val Arg Leu Ala Leu Glu Asp Glu Lys Gly Asn Arg Gln Asn
 450 455 460

Ser Gly Val Val Glu Ile Thr Val Gln Gln Asp Arg Lys Ile Glu Leu
 465 470 475 480

Ile Val Asn Asn Ile Ala Asn Pro Glu Glu Asn Asn His Ser His Glu
 485 490 495

Ala Ser Ala Gln Ala Asp Gly Val Asp Gly Val Val Met Asp Leu Asp
 500 505 510

Val Thr Asp Ser Phe Gly Asp Asn Thr Asp Arg Asn Gly Asp Ala Leu
 515 520 525

Pro Glu Asp Asn Leu Thr Pro Gln Leu Tyr Asp Ala Gln Asp Lys Arg
 530 535 540

Val Thr Leu Thr Asn Lys Pro Cys Ser Thr Asp Asn Pro Cys Val Phe
 545 550 555 560

Ile Ala Lys Gln Asp Lys Glu Lys Gly Thr Val Thr Leu Ser Ser Thr
 565 570 575

Leu Pro Gly Thr Tyr Arg Trp Lys Ala Lys Ala Ala Pro Tyr Asp Asp
 580 585 590

Ser Asn Tyr Val Asp Val Thr Phe Leu Gly Ala Glu Ile Gly Gly Leu
 595 600 605

Asn Ala Phe Ile Tyr Arg Val Gly Ala Ala Lys Pro Ser Asn Leu Ile
 610 615 620

Gly Lys Asp Lys Glu Pro Leu Pro Ser Thr Thr Phe Ile Asp Leu Phe
 625 630 635 640

Tyr Gly Ala Thr Thr Ile Lys Thr Val Ser Ser Ser Arg Ser Lys Asn
 645 650 655

Leu Thr Lys Arg Trp Cys Ser Thr Thr Thr Ser Gly Asn Leu Pro Ala
 660 665 670

70

Arg Ala Ser Met Val Ser Gly Cys Thr Gly Glu His Ser Asn Glu Asp
 675 680 685

Ile Val Ile Pro Ala Thr Asn Arg Glu Ala Ala Gln Thr Tyr Gly Ala
 690 695 700

Gln Ala Gly Asp Gly Leu Gln Gly Tyr Gly Leu Arg Val Leu Tyr Thr
 705 710 715 720

Lys Lys

<210> 32
 <211> 319
 <212> PRT
 <213> Escherichia coli
 <400> 32

Met Lys Gln Asp Lys Arg Arg Gly Leu Thr Arg Ile Ala Leu Ala Leu
 1 5 10 15

Ala Leu Ala Gly Tyr Cys Val Ala Pro Val Ala Leu Ala Glu Asp Ser
 20 25 30

Ala Trp Val Asp Ser Gly Glu Thr Asn Ile Phe Gln Gly Thr Ile Pro
 35 40 45

Trp Leu Tyr Ser Glu Gly Gly Ser Ala Thr Thr Asp Ala Asp Arg Val
 50 55 60

Thr Leu Thr Ser Asp Leu Lys Gly Ala Arg Pro Gln Gly Met Lys Arg
 65 70 75 80

Thr Ser Val Phe Thr Arg Val Ile Asn Ile Gly Asp Thr Glu Gly Asp
 85 90 95

Val Asp Leu Gly Gly Leu Gly Asp Asn Ala Lys Thr Ile Asp Thr Ile
 100 105 110

Arg Trp Met Ser Tyr Lys Asp Ala Gln Gly Gly Asp Pro Lys Glu Leu
 115 120 125

Ala Thr Lys Val Thr Ser Tyr Thr Leu Thr Asp Ala Asp Arg Gly Arg
 130 135 140

Tyr Ile Gly Ile Glu Ile Thr Pro Thr Thr Gln Thr Gly Thr Pro Asn
 145 150 155 160

Val Gly Thr Ala Leu His Leu Tyr Asp Val Ser Thr Ala Ser Gly Gly
 165 170 175

Gly Ser Asp Ser Asp Asn Val Ala Pro Gly Pro Val Val Asn Gln Asn
 180 185 190

Leu Lys Val Ala Ile Phe Val Asp Gly Thr Ser Ile Asn Leu Ile Asn
 195 200 205

Gly Ser Thr Pro Ile Glu Leu Gly Lys Thr Tyr Val Ala Lys Leu Tyr
 210 215 220

Ser Asp Glu Asn Lys Asn Gly Lys Phe Asp Ala Gly Thr Asp Ala Asp
 225 230 235 240

Val Thr Ala Asn Tyr Asp Phe Arg Trp Val Leu Ser Gly Ser Ser Gln
 245 250 255

Gln Leu Gly Thr Ser Gly Gly Ile Val Asn Ser Ser Phe Asp Asn Asn
 260 265 270

Asn Leu Val Ile Pro Ala Thr Asn Asp Glu Ala Arg Thr Asn Leu Asn
 275 280 285

Gly Pro Ala Arg Asp Gly Lys Glu Ala Leu Ser Ile Pro Thr Asn Gly
 290 295 300

Asp Gly Val Gln Gly Tyr Lys Leu His Ile Ile Tyr Lys His Lys
 305 310 315

<210> 33

<211> 629

<212> PRT

<213> Escherichia coli

<400> 33

Met Lys Lys Val Leu Thr Leu Ser Leu Leu Ala Leu Cys Val Ser His
 1 5 10 15

Ser Ala Val Ala Ala Asn Tyr Thr Phe Asn Asn Asp Asn Ile Ala Leu
 20 25 30

Ser Phe Asp Asp Thr Asn Ser Thr Ile Val Leu Lys Asp Arg Arg Thr
 35 40 45

Asn His Pro Ile Thr Pro Gln Glu Leu Phe Phe Leu Thr Leu Pro Asp
 50 55 60

Glu Thr Lys Ile His Thr Ala Asp Phe Lys Ile Lys His Ile Lys Lys
 65 70 75 80

Gln Asp Asn Ala Ile Val Ile Asp Phe Thr Arg Pro Asp Phe Asn Val
 85 90 95

Thr Val Gln Leu Asn Leu Val Lys Gly Lys Tyr Ala Ser Ile Asp Tyr
 100 105 110

Thr Ile Ala Ala Val Gly Gln Pro Arg Asp Val Ala Lys Ile Thr Phe
 115 120 125

Phe Pro Thr Lys Lys Gln Phe Gln Ala Pro Tyr Val Asp Gly Ala Ile
 130 135 140

Thr Ser Ser Pro Ile Ile Ala Asp Ser Phe Phe Ile Leu Pro Asn Lys
 145 150 155 160

Pro Ile Val Asn Thr Tyr Ala Tyr Glu Ala Thr Thr Asn Leu Asn Val
 165 170 175

Glu Leu Lys Thr Pro Ile Gln Pro Glu Thr Pro Val Ser Phe Thr Thr
 180 185 190

Trp Phe Gly Thr Phe Pro Glu Thr Ser Gln Leu Arg Arg Ser Val Asn
 195 200 205

Gln Phe Ile Asn Ala Val Arg Pro Arg Pro Tyr Lys Pro Tyr Leu His
 210 215 220

Tyr Asn Ser Trp Met Asp Ile Gly Phe Phe Thr Pro Tyr Thr Glu Gln
 225 230 235 240

Asp Val Leu Gly Arg Met Asp Glu Trp Asn Lys Glu Phe Ile Ser Gly
 245 250 255

Arg Gly Val Ala Leu Asp Ala Phe Leu Leu Asp Asp Gly Trp Asp Asp
 260 265 270

Leu Thr Gly Arg Trp Leu Phe Gly Pro Ala Phe Ser Asn Gly Phe Ser
 275 280 285

Lys Val Arg Glu Lys Ala Asp Ser Leu His Ser Ser Val Gly Leu Trp
 290 295 300

Leu Ser Pro Trp Gly Gly Tyr Asn Lys Pro Gln Arg Arg Ser Arg Phe
 305 310 315 320

Ala Cys Lys Arg Val Trp Val Arg Asn Arg Gly Arg Gln Ala Gly Ala
 325 330 335

Phe Gly Ser Glu Leu Leu Lys Asn Phe Asn Glu Gln Ile Ile Asn Leu
 340 345 350

Ile Lys Asn Glu His Ile Thr Ser Phe Lys Leu Asp Gly Met Gly Asn
 355 360 365

Ala Ser Ser His Ile Lys Gly Ser Pro Phe Ala Ser Asp Phe Asp Ala
 370 375 380

Ser Ile Ala Leu Leu His Asn Met Arg Arg Ala Asn Pro Asn Leu Phe
 385 390 395 400

Ile Asn Leu Thr Thr Gly Thr Asn Ala Ser Pro Ser Trp Leu Phe Tyr
 405 410 415

Ala Asp Ser Ile Trp Arg Gln Gly Asp Asp Ile Asn Leu Tyr Gly Pro
 420 425 430

Gly Thr Pro Val Gln Gln Trp Ile Thr Tyr Arg Asp Ala Glu Thr Tyr
 435 440 445

Arg Ser Ile Val Arg Lys Gly Pro Leu Phe Pro Leu Asn Ser Leu Met
 450 455 460

Tyr His Gly Ile Val Ser Ala Glu Asn Ala Tyr Tyr Gly Leu Glu Lys
 465 470 475 480

74

Val Gln Thr Asp Ser Asp Phe Ala Asp Gln Val Trp Ser Tyr Phe Ala
 485 490 495

Thr Gly Thr Gln Leu Gln Glu Leu Tyr Ile Thr Pro Ser Met Leu Asn
 500 505 510

Lys Val Lys Trp Asp Thr Leu Ala Lys Ala Ala Lys Trp Ser Lys Glu
 515 520 525

Asn Ala Ser Val Leu Val Asp Thr His Trp Ile Gly Gly Asp Pro Thr
 530 535 540

Ala Leu Ala Val Tyr Gly Trp Ala Ser Trp Ser Lys Asp Lys Ala Ile
 545 550 555 560

Leu Gly Leu Arg Asn Pro Ser Asp Lys Pro Gln Thr Tyr Tyr Leu Asp
 565 570 575

Leu Ala Lys Asp Phe Glu Ile Pro Ala Gly Asn Ala Ala Gln Phe Ser
 580 585 590

Leu Lys Ala Val Tyr Gly Ser Asn Lys Thr Val Pro Val Glu Tyr Lys
 595 600 605

Asn Ala Thr Val Ile Thr Leu Gln Pro Leu Glu Thr Leu Val Phe Glu
 610 615 620

Ala Val Thr Ile Asn
 625

<210> 34

<211> 1778

<212> PRT

<213> Escherichia coli

<400> 34

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr
 1 5 10 15

Thr Val Ala Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
 20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Leu Leu Ser Ser
 35 40 45

75

Phe Gly Ala Ser Ala Asp Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly
50 55 60

Asp Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly Ala Lys
65 70 75 80

Ala Asn Thr Phe Met Asn Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr
85 90 95

Asp Ala Ile Ala Glu Gly Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr
100 105 110

Leu Ala Thr Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala Lys Ala
115 120 125

Met Gly Asp Arg Ser Val Ala Leu Gly Ala Ser Ser Val Ala Asn Gly
130 135 140

Asp Arg Ser Met Ala Phe Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr
145 150 155 160

Ser Leu Ala Ile Gly Asp Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile
165 170 175

Ala Leu Gly Asn Thr Ala Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu
180 185 190

Gly Asp Asn Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala
195 200 205

Ser Ser Lys Ala Gly Gly Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser
210 215 220

Thr Ala Asn Ser Thr Gly Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser
225 230 235 240

Ser Asn Asp Asn Ala Ile Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly
245 250 255

Val Asn Ser Met Ala Leu Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser
260 265 270

76

Ser Ile Ala Leu Gly Asn Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile
275 280 285

Ala Leu Gly Gln Gly Ser Ile Ala Ser Lys Val Asn Ser Ile Ala Leu
290 295 300

Gly Ser Asn Ser Leu Ser Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu
305 310 315 320

Gly Ser Ala Ala Gly Gly Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser
325 330 335

Arg Ala Asn Gly Asn Asp Ser Val Ala Ile Gly Val Gly Ala Ala Ala
340 345 350

Ala Thr Asp Asn Ser Val Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala
355 360 365

Ser Asn Thr Val Ser Val Gly Asn Ser Ala Thr Lys Arg Lys Ile Val
370 375 380

Asn Met Ala Ala Gly Ala Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn
385 390 395 400

Gly Ser Gln Leu Tyr Thr Ile Ser Asp Ser Val Ala Lys Arg Leu Gly
405 410 415

Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala Val Ser Tyr
420 425 430

Ala Leu Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly
435 440 445

Ile Asp Asn Asn Thr Leu Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser
450 455 460

Ala Asn His Gly Ala Asn Ala Thr Asn Lys Ile Thr Asn Val Ala Lys
465 470 475 480

Gly Thr Val Ser Ala Thr Ser Thr Asp Val Val Asn Gly Ser Gln Leu
485 490 495

Tyr Asp Leu Gln Gln Asp Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser

500	505	510
Ala Ala His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala 515 520 525		
Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu 530 535 540		
Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr 545 550 555 560		
Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly 565 570 575		
Asp Asp Ser Leu Leu Trp Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala 580 585 590		
His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn 595 600 605		
Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr 610 615 620		
Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr 625 630 635 640		
Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp 645 650 655		
Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly 660 665 670		
Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr 675 680 685		
Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn 690 695 700		
Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn 705 710 715 720		
Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu 725 730 735		

Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp
 740 745 750

Ala Thr Ser Lys Ile Thr Asn Val Lys Ala Gly Asp Leu Thr Ala Gly
 755 760 765

Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn
 770 775 780

Val Ser Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn
 785 790 795 800

Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe
 805 810 815

Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys
 820 825 830

Ala Gly Asp Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln
 835 840 845

Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Ile Thr
 850 855 860

Asn Leu Thr Asp Ser Val Gly Asp Leu Lys Asp Asp Ser Leu Leu Trp
 865 870 875 880

Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr
 885 890 895

Ser Lys Ile Thr Asn Leu Leu Ala Gly Lys Ile Ser Ser Asn Ser Thr
 900 905 910

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val Ala Asp Ser Phe Thr
 915 920 925

Ser Tyr Leu Gly Gly Gly Ala Asp Ile Ser Asp Thr Gly Val Leu Ser
 930 935 940

Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp
 945 950 955 960

Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr Ser Leu Gly Asp Ala
 965 970 975

Leu Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Ile
 980 985 990

Asn Asn Ala Pro Ser Val Ile Thr Asp Val Ala Asn Gly Ala Val Ser
 995 1000 1005

Ser Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val
 1010 1015 1020

Ser Asp Tyr Ile Ala Asp Ala Leu Gly Gly Asn Ala Val Val Asn
 1025 1030 1035

Thr Asp Gly Ser Ile Thr Thr Pro Thr Tyr Ala Ile Ala Gly Gly
 1040 1045 1050

Ser Tyr Asn Asn Val Gly Asp Ala Leu Glu Ala Ile Asp Thr Thr
 1055 1060 1065

Leu Asp Asp Ala Leu Leu Trp Asp Thr Thr Ala Asn Gly Gly Asn
 1070 1075 1080

Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val
 1085 1090 1095

Ile Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp
 1100 1105 1110

Ala Ile Asn Gly Ser Gln Leu Tyr Ser Thr Asn Lys Tyr Ile Ala
 1115 1120 1125

Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile
 1130 1135 1140

Thr Ala Pro Thr Tyr Thr Ile Ala Asn Thr Asp Tyr Asn Asn Val
 1145 1150 1155

Gly Glu Ala Leu Asp Ala Leu Asp Asn Asn Ala Leu Leu Trp Asp
 1160 1165 1170

Glu Asp Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Asn Ala Ser
 1175 1180 1185
 Lys Ile Thr Asn Val Ala Ala Gly Asp Leu Ser Thr Thr Ser Thr
 1190 1195 1200
 Asp Ala Val Asn Gly Ser Gln Leu Asn Ala Thr Asn Ile Leu Val
 1205 1210 1215
 Thr Gln Asn Ser Gln Met Ile Asn Gln Leu Ala Gly Asn Thr Ser
 1220 1225 1230
 Glu Thr Tyr Ile Glu Glu Asn Gly Ala Gly Ile Asn Tyr Val Arg
 1235 1240 1245
 Thr Asn Asp Ser Gly Leu Ala Phe Asn Asp Ala Ser Ala Ser Gly
 1250 1255 1260
 Ile Gly Ala Thr Ala Val Gly Tyr Asn Ala Val Ala Ser His Ala
 1265 1270 1275
 Ser Ser Val Ala Ile Gly Gln Asp Ser Ile Ser Glu Val Asp Thr
 1280 1285 1290
 Gly Ile Ala Leu Gly Ser Ser Ser Val Ser Ser Arg Val Ile Val
 1295 1300 1305
 Lys Gly Thr Arg Asn Thr Ser Val Ser Glu Glu Gly Val Val Ile
 1310 1315 1320
 Gly Tyr Asp Thr Thr Asp Gly Glu Leu Leu Gly Ala Leu Ser Ile
 1325 1330 1335
 Gly Asp Asp Gly Lys Tyr Arg Gln Ile Ile Asn Val Ala Asp Gly
 1340 1345 1350
 Ser Glu Ala His Asp Ala Val Thr Val Arg Gln Leu Gln Asn Ala
 1355 1360 1365
 Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr Tyr His Ala Asn
 1370 1375 1380
 Ser Thr Ala Glu Asp Ser Leu Ala Val Gly Glu Asp Ser Leu Ala

1385	1390	1395
Met Gly Ala Lys Thr Ile Val	Asn Gly Asn Ala Gly	Ile Gly Ile
1400	1405	1410
Gly Leu Asn Thr Leu Val Leu	Ala Asp Ala Ile Asn	Gly Ile Ala
1415	1420	1425
Ile Gly Ser Asn Ala Arg Ala	Asn His Ala Asp Ser	Ile Ala Met
1430	1435	1440
Gly Asn Gly Ser Gln Thr Thr	Arg Gly Ala Gln Thr	Asn Tyr Thr
1445	1450	1455
Ala Tyr Asn Met Asp Ala Pro	Gln Asn Ser Val Gly	Glu Phe Ser
1460	1465	1470
Val Gly Ser Glu Asp Gly Gln	Arg Gln Ile Thr Asn	Val Ala Ala
1475	1480	1485
Gly Ser Ala Asp Thr Asp Ala	Val Asn Val Gly Gln	Leu Lys Val
1490	1495	1500
Thr Asp Ala Gln Val Ser Gln	Asn Thr Gln Ser Ile	Thr Asn Leu
1505	1510	1515
Asn Thr Gln Val Thr Asn Leu	Asp Thr Arg Val Thr	Asn Ile Glu
1520	1525	1530
Asn Gly Ile Gly Asp Ile Val	Thr Thr Gly Ser Thr	Lys Tyr Phe
1535	1540	1545
Lys Thr Asn Thr Asp Gly Ala	Asp Ala Asn Ala Gln	Gly Lys Asp
1550	1555	1560
Ser Val Ala Ile Gly Ser Gly	Ser Ile Ala Ala Ala	Asp Asn Ser
1565	1570	1575
Val Ala Leu Gly Thr Gly Ser	Val Ala Asp Glu Glu	Asn Thr Ile
1580	1585	1590
Ser Val Gly Ser Ser Thr Asn	Gln Arg Arg Ile Thr	Asn Val Ala
1595	1600	1605

Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser Gln Leu Lys
 1610 1615 1620

Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp Thr Lys Ala Asp Gly
 1625 1630 1635

Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly Gly Asn Ser Gly
 1640 1645 1650

Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn Asp
 1655 1660 1665

Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys
 1670 1675 1680

Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser
 1685 1690 1695

Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala
 1700 1705 1710

Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala
 1715 1720 1725

Ser Ile Gly Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu
 1730 1735 1740

Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu
 1745 1750 1755

Gln Gly Ser Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly
 1760 1765 1770

Ala Gly Ile Gln Trp
 1775

<210> 35

<211> 227

<212> PRT

<213> Escherichia coli

<400> 35

Met Asn Leu Lys Lys Thr Leu Leu Ser Val Leu Met Ile Leu Gln Leu

83

1	5	10	15
Cys	Leu	Leu	Val
20	Gly	Cys	Asp
Tyr	Ile	Glu	Lys
25	Ala	Ser	Lys
30	Val	Asp	
Asp	Leu	Val	Thr
35	Gln	Gln	Glu
40	Leu	Gln	Lys
45	Ser	Lys	Ile
Glu	Ala	Leu	
Glu	Lys	Gln	Gln
50	Glu	Leu	Asp
55	Lys	Arg	Lys
60	Ile	Glu	His
Phe	Glu	Lys	
Gln	Gln	Thr	Thr
65	Ile	Ile	Asn
70	Ser	Thr	Lys
75	Thr	Leu	Ala
80	Gly	Val	Val
Lys	Ala	Val	Lys
85	Asn	Lys	Gln
90	Asp	Glu	Phe
95	Val	Phe	Thr
Glu	Phe	Asn	
Pro	Ala	Gln	Thr
100	Gln	Tyr	Phe
105	Ile	Leu	Asn
110	Asn	Gly	Ser
Val	Gly	Leu	
Ala	Gly	Lys	Ile
115	Leu	Ser	Ile
120	Asp	Ala	Val
125	Glu	Asn	Gly
Ser	Val	Ile	
Arg	Ile	Ser	Leu
130	Val	Asn	Leu
135	Leu	Ser	Val
140	Pro	Val	Ser
145	Asn	Met	Gly
Phe	Tyr	Ala	Thr
150	Trp	Gly	Gly
155	Glu	Lys	Pro
160	Thr	Asp	Ile
Ala	Lys	Trp	Gln
165	Gln	Leu	Leu
170	Phe	Ser	Thr
175	Ala	Met	Asn
Lys	Leu	Leu	Pro
180	Gly	Gln	Trp
185	Gln	Asp	Ile
190	Asn	Leu	Thr
Val	Ser	Pro	Asn
195	Asn	Leu	Lys
200	Tyr	Leu	Lys
205	Leu	Ala	Ile
Asn	Met	Ala	
Asn	Ile	Gln	Phe
210	Asp	Arg	Leu
215	Gln	Pro	Ala
220	Glu	Ser	Pro
Gln	Arg	Lys	
Asn	Lys	Lys	
225			

<210> 36
 <211> 1109
 <212> PRT
 <213> Escherichia coli
 <400> 36

Met Lys Arg Val Val Arg Leu Leu Gly Val Gly Leu Leu Leu Leu Val
 1 5 10 15

Val Leu Leu Leu Ile Leu Phe Val Leu Ala Gln Thr Thr Pro Leu Ile
 20 25 30

Ser Ala Gln Asp Glu His Ala Val Trp Leu Arg Leu Leu Ile Thr Ala
 35 40 45

Ile Val Ile Cys Leu Leu Ser Met Cys Ile Phe Phe Leu Phe Ser Phe
 50 55 60

Arg Gln Asn Glu Ala Ser Thr Ile Ser Leu Tyr Ala Gln Pro Thr Asp
 65 70 75 80

Ile Lys Glu Ile Asn Thr Glu Gln Pro Asn Tyr Ala Ser Leu Leu Thr
 85 90 95

Ile Tyr Leu Arg Asp Arg Tyr Gly Pro Phe Trp Arg Arg Lys Val Arg
 100 105 110

Leu Leu Leu Val Thr Gly Glu Pro Glu Gln Ala Glu Ala Ile Ala Pro
 115 120 125

Gly Leu Thr Gly Gln His Trp Leu Glu Gly Asp His Thr Val Leu Ile
 130 135 140

Tyr Gly Gly Arg Pro Thr Ala Glu Pro Asp Val Thr Leu Leu Thr Ala
 145 150 155 160

Leu Lys Lys Leu Arg Arg Ser Arg Pro Leu Asp Gly Ile Ile Trp Ala
 165 170 175

Leu Thr Glu Glu Gln Ser Arg Gln Thr Ala Gln Leu Asp Lys Gly Trp
 180 185 190

Arg Gly Leu Ile Asn Gly Gly Lys Arg Leu Gly Phe Gln Ala Pro Leu

195	200	205
Tyr Leu Trp Gln Val Cys Asp Asp Gly Asp Tyr Gln Thr Gly Arg Pro 210 215 220		
Leu Gln Ser Val Gly Cys Leu Leu Pro Glu Arg Cys Thr Pro Glu Gln 225 230 235 240		
Leu Ala Val Met Leu Glu Ala Ala Ala Asp Gly Thr Gly His Val Ala 245 250 255		
Ala Thr Asp Arg Tyr Arg Met Phe Ser Ala Ala Ser Gly Ser Tyr Pro 260 265 270		
Cys Arg Ala Gly Tyr Cys Ser Leu Ala Asp Arg Pro Glu Thr Ala Ala 275 280 285		
Gly Arg Arg Arg Ile Phe Phe Pro Ala Pro Ala Arg Pro Asp Val Gln 290 295 300		
Pro Ala Ala Cys Arg Arg Ala Gly Gly Gln His Leu Met Gln Trp Leu 305 310 315 320		
Pro Ser Pro Val Trp Ala Gly Val Thr Val Ile Thr Arg Ala Gly Ala 325 330 335		
Arg Trp Val Phe Leu Trp Leu Arg Thr Ala Leu Met Ser Ala Val Cys 340 345 350		
Val Leu Val Ile Trp Gly Ala Gly Met Thr Thr Ser Phe Phe Ala Asn 355 360 365		
Arg Ala Leu Val Gln Glu Thr Gly Ile Gln Thr Ala Arg Ala Leu Asp 370 375 380		
Thr Arg Leu Pro Leu Ala Glu Gln Leu Val Ala Leu His Thr Leu Gln 385 390 395 400		
Gly Glu Leu Glu Arg Leu Gln Tyr Arg Ile Arg Glu Gly Ala Pro Trp 405 410 415		
Tyr Gln Arg Phe Gly Leu Glu Arg Asn Gln Gln Leu Leu Ala Ala Ala 420 425 430		

Phe Pro Gly Tyr Ala Gln Ala Ala Asn Arg Leu Val Arg Asp Val Ala
 435 440 445

Val Asp His Leu Gln Gln Gln Leu Asn Ala Phe Val Ala Leu Pro Pro
 450 455 460

Asn Ser Pro Gln Arg Thr Ala Thr Gly Glu Gln Arg Tyr Lys Gln Leu
 465 470 475 480

Lys Ala Leu Leu Met Thr Ser Arg Pro Glu Lys Ala Asp Ala Ala Phe
 485 490 495

Phe Ser Thr Thr Leu Met Ala Asp Gly Leu Arg Tyr Glu Asn Ile Pro
 500 505 510

Glu Gly Val Arg Gln Ser Val Leu Pro Ser Leu Leu Thr Phe Trp Thr
 515 520 525

Ala Asn Leu Pro Glu His Pro Gln Trp Lys Thr Ser Pro Pro Pro Glu
 530 535 540

Leu Thr Gly Ala Val Arg Lys Ile Leu Leu Arg Gln Ile Gly Val Arg
 545 550 555 560

Asn Ala Glu Asn Thr Leu Tyr Gln Asn Val Leu Gln Gln Val Ser Arg
 565 570 575

Asn Tyr Ala Asp Met Thr Leu Ala Asp Met Thr Gly Asp Thr Leu Thr
 580 585 590

Glu Ser Leu Phe Ser Thr Glu Gln Thr Val Pro Gly Met Phe Thr Arg
 595 600 605

Gln Ala Trp Glu Gly Gln Val Arg Glu Ala Ile Glu Gln Val Val Thr
 610 615 620

Ala Arg Arg Glu Glu Ile Asp Trp Val Leu Ser Asp Arg Gln Gln Asp
 625 630 635 640

Thr Ser Ala Asp Ile Ser Pro Asp Thr Leu Arg Asn Arg Leu Thr Ser
 645 650 655

Arg Tyr Phe Thr Asp Phe Ala Gly Ser Trp Leu Ala Phe Leu Asn Ser
 660 665 670

Ile His Trp Lys Lys Glu Asp Ser Leu Ser Gly Ile Leu Asp Gln Leu
 675 680 685

Thr Leu Met Ala Asp Ala Arg Gln Ser Pro Leu Ile Ala Leu Thr Asp
 690 695 700

Thr Leu Ala Trp Gln Ala Ala Thr Gly Arg Glu Asn Arg Gly Leu Ser
 705 710 715 720

Asp Ser Leu Ala Lys Ser Ala Gln Glu Leu Phe Asn Gly Lys Glu Lys
 725 730 735

Thr Pro Gln Gln Ser Arg Glu Gly Asp Asp Val Pro Val Gly Pro Leu
 740 745 750

Asp Lys Thr Phe Thr Pro Leu Leu Arg Leu Leu Gly Asp Lys Ala Gly
 755 760 765

Gly Gly Asp Ser Gln Leu Ser Leu Gln Thr Tyr Leu Thr Arg Val Thr
 770 775 780

Arg Val Arg Leu Lys Leu Gln Gln Val Thr Asn Ala Pro Asp Pro Gln
 785 790 795 800

Glu Met Thr Gln Gln Leu Ala Gln Thr Val Leu Gln Gly Lys Thr Val
 805 810 815

Asp Leu Thr Asp Thr Arg Asp Tyr Gly Arg Leu Ile Ala Ala Ser Leu
 820 825 830

Gly Glu Glu Trp Ser Gly Phe Gly Gln Ala Leu Phe Val Arg Pro Val
 835 840 845

Glu Gln Ser Trp Arg Gln Val Leu Thr Pro Ala Ala Asp Ser Leu Asn
 850 855 860

Arg Gln Trp Gln Arg Ala Ile Val Ser His Trp Asn Gln Asp Phe Ala
 865 870 875 880

Gly Arg Tyr Pro Phe Lys Ala Ser Gln Asn Asp Ala Ser Leu Pro Leu
 885 890 895

Leu Ala Gln Tyr Leu Arg Asp Asp Gly Arg Ile Asn Leu Phe Ile Ala
 900 905 910

Ala Asn Leu Ser Gly Val Leu Lys Arg Glu Gly Arg Tyr Trp Val Ala
 915 920 925

Asp Ala Met Asn Thr Gln Gly Leu Thr Val Asn Pro Asp Phe Ile Arg
 930 935 940

Ala Leu Asn Arg Leu Arg Asp Val Ala Asp Thr Ala Phe Ala Ser Gly
 945 950 955 960

Asp Ala Gly Ile His Phe Glu Leu Arg Ala Lys Pro Ala Arg Asp Val
 965 970 975

Met Lys Thr His Leu Val Ile Asp Gly Gln Glu Leu Glu Tyr Phe Asn
 980 985 990

Gln Lys Glu Arg Trp Gln Arg Phe Asn Trp Pro Asp Glu Gln Trp Gln
 995 1000 1005

Pro Gly Ala Ser Leu Ser Trp Thr Ser Thr Gln Ala Met Glu Arg
 1010 1015 1020

Ile Leu Ala Asp Tyr Arg Gly Ser Trp Ser Leu Ile Arg Leu Leu
 1025 1030 1035

Glu Gln Ala Gln Val Thr Pro Val Asp Ser Ser Thr Phe Lys Val
 1040 1045 1050

Val Trp Lys Ala Gln Asp Gly Leu Pro Leu Asn Tyr Leu Leu Arg
 1055 1060 1065

Val Glu Gln Gly Lys Gly Pro Leu Ala Leu Leu Glu Leu Lys Asn
 1070 1075 1080

Phe Arg Leu Pro Gly Gln Val Phe Leu Thr Gly Lys Ser Met Lys
 1085 1090 1095

Asp Val Glu Glu Tyr Gly Glu Asp Ala Asp Glu

1100

1105

<210> 37
 <211> 178
 <212> PRT
 <213> Escherichia coli
 <400> 37

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
 1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
 20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
 35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
 50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
 65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
 85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
 100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
 115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
 130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
 145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
 165 170 175

Asp Lys

<210> 38
 <211> 280
 <212> PRT
 <213> Escherichia coli
 <400> 38

Met Ile Ser Gly Gly Asn Met Leu Lys Glu Trp Met Ile Phe Thr Cys
 1 5 10 15

Ser Leu Leu Thr Leu Ala Gly Ala Ser Leu Pro Leu Ser Gly Cys Ile
 20 25 30

Ser Arg Gly Gln Glu Ser Ile Ser Glu Gly Ala Ala Phe Gly Ala Gly
 35 40 45

Ile Leu Arg Glu Pro Gly Ala Thr Lys Lys Ala Asp Thr Lys Asp Leu
 50 55 60

Asn Val Pro Pro Pro Val Tyr Gly Pro Pro Gln Val Ile Phe Arg Ile
 65 70 75 80

Asp Asp Asn Arg Tyr Phe Thr Leu Glu Asn Tyr Thr His Cys Glu Asn
 85 90 95

Gly Gln Thr Phe Tyr Asn Asn Lys Ala Lys Asn Ile His Val Lys Ile
 100 105 110

Leu Asp Ala Ser Gly Tyr Leu Phe Lys Gly Arg Leu Phe Trp Leu Ser
 115 120 125

Thr Arg Asp Asp Phe Leu Ala Phe Pro Ala Thr Leu Asn Thr Arg His
 130 135 140

Ala Ser Cys Met Gly Ser Asn Lys Gly Cys Met Asn Ala Val Ile Val
 145 150 155 160

Thr Thr Asp Gly Gly Lys Arg Arg Ser Gly Val Pro Tyr Gly Ser Tyr
 165 170 175

Thr Gln Asn Pro Thr Gly Ala Thr Arg Asp Tyr Asp Met Leu Val Met
 180 185 190

Asn Asp Gly Phe Tyr Leu Leu Arg Tyr Arg Gly Gly Gln Gly Arg Phe
 195 200 205

Ser Pro Val Ile Leu Arg Trp Ile Leu Ser Thr Glu Asp Ser Ser Gly
 210 215 220

Val Val Arg Ser Glu Asp Ala Tyr Glu Leu Phe Arg Pro Gly Glu Glu
 225 230 235 240

Val Pro Ser Thr Gly Phe Tyr Lys Ile Asp Leu Ser Arg Phe Tyr Pro
 245 250 255

Lys Asn Asn Val Met Glu Met Gln Cys Asp Arg Thr Leu Glu Pro Val
 260 265 270

Gln Pro Ser Glu Ser Lys Ile Gln
 275 280

<210> 39
 <211> 501
 <212> PRT
 <213> Escherichia coli
 <400> 39

Met Glu His Val Ser Ile Lys Thr Leu Tyr His Leu Leu Cys Cys Met
 1 5 10 15

Leu Leu Phe Ile Ser Ala Met Cys Ala Leu Ala Gln Glu His Glu Pro
 20 25 30

Ile Gly Ala Gln Asp Glu Arg Leu Ser Thr Leu Ile His Gln Arg Met
 35 40 45

Gln Glu Ala Lys Val Pro Ala Leu Ser Val Ser Val Thr Ile Lys Gly
 50 55 60

Val Arg Gln Arg Phe Val Tyr Gly Val Ala Asp Val Ala Ser Gln Lys
 65 70 75 80

Ala Asn Thr Leu Asp Thr Val Tyr Glu Leu Gly Ser Met Ser Lys Ala
 85 90 95

Phe Thr Gly Leu Val Val Gln Ile Leu Ile Gln Glu Gly Arg Leu Arg
 100 105 110

Gln Gly Asp Asp Ile Ile Thr Tyr Leu Pro Glu Met Arg Leu Asn Tyr
 115 120 125

Gln Gly Lys Pro Ala Ser Leu Thr Val Ala Asp Phe Leu Tyr His Thr
 130 135 140

Ser Gly Leu Pro Phe Ser Thr Leu Ala Arg Leu Glu Asn Pro Met Pro
 145 150 155 160

Gly Ser Ala Val Ala Gln Gln Leu Arg Asn Glu Asn Leu Leu Phe Ala
 165 170 175

Pro Gly Ala Lys Phe Ser Tyr Ala Ser Ala Asn Tyr Asp Val Leu Gly
 180 185 190

Ala Val Ile Glu Asn Val Thr Gly Lys Thr Phe Thr Glu Val Ile Ala
 195 200 205

Glu Arg Leu Thr Gln Pro Leu Gly Met Ser Ala Thr Val Ala Val Lys
 210 215 220

Gly Asp Glu Ile Ile Val Asn Lys Ala Ser Gly Tyr Lys Leu Gly Phe
 225 230 235 240

Gly Lys Pro Val Leu Phe His Ala Pro Leu Ala Arg Asn His Val Pro
 245 250 255

Ala Ala Tyr Ile His Ser Thr Leu Pro Asp Met Glu Ile Trp Ile Asp
 260 265 270

Ala Trp Leu His Arg Lys Ala Leu Pro Ala Thr Leu Arg Glu Ala Met
 275 280 285

Ser Asn Ser Trp Arg Gly Asn Ser Asp Val Pro Leu Ala Ala Asp Asn
 290 295 300

Arg Ile Leu Tyr Ala Ser Gly Trp Phe Ile Asp Gln Asn Gln Gly Pro
 305 310 315 320

Tyr Ile Ser His Gly Gly Gln Asn Pro Asn Phe Ser Ser Cys Ile Ala
 325 330 335

Leu Arg Pro Asp Gln Gln Ile Gly Ile Val Ala Leu Ala Asn Met Asn
 340 345 350

Ser Asn Leu Ile Leu Gln Leu Cys Ala Asp Ile Asp Asn Tyr Leu Arg
 355 360 365

Ile Gly Lys Tyr Ala Asp Gly Ala Gly Asp Ala Ile Thr Ala Thr Asp
 370 375 380

Thr Leu Phe Val Tyr Leu Thr Leu Leu Leu Cys Phe Trp Gly Ala Val
 385 390 395 400

Val Val Val Arg Gly Ala Phe Arg Val Tyr Arg Ala Thr Ala His Gly
 405 410 415

Pro Gly Lys Gln Gln Arg Leu Arg Leu Arg Val Arg Asp Tyr Ile Ile
 420 425 430

Ala Leu Ala Val Pro Gly Leu Val Ala Ala Met Leu Tyr Val Ala Pro
 435 440 445

Gly Ile Leu Ser Pro Gly Leu Asp Trp Arg Phe Ile Leu Val Trp Gly
 450 455 460

Pro Ser Ser Val Leu Ala Ile Pro Phe Gly Ile Ile Leu Leu Ala Phe
 465 470 475 480

Val Leu Thr Leu Asn His Gln Ile Lys Arg Ile Leu Leu His Asn Lys
 485 490 495

Glu Trp Asp Asp Glu
 500

<210> 40

<211> 682

<212> PRT

<213> Escherichia coli

<400> 40

Met Lys Asn Lys Tyr Ile Ile Ala Pro Gly Ile Ala Val Met Cys Ser
 1 5 10 15

Ala Val Ile Ser Ser Gly Tyr Ala Ser Ser Asp Lys Lys Glu Asp Thr
 20 25 30

Leu Val Val Thr Ala Ser Gly Phe Thr Gln Gln Leu Arg Asn Ala Pro
 35 40 45

Ala Ser Val Ser Val Ile Thr Ser Glu Gln Leu Gln Lys Lys Pro Val
 50 55 60

Ser Asp Leu Val Asp Ala Val Lys Asp Val Glu Gly Ile Ser Ile Thr
 65 70 75 80

Gly Gly Asn Glu Lys Pro Asp Ile Ser Ile Arg Gly Leu Ser Gly Asp
 85 90 95

Tyr Thr Leu Ile Leu Val Asp Gly Arg Arg Gln Ser Gly Arg Glu Ser
 100 105 110

Arg Pro Asn Gly Ser Gly Gly Phe Glu Ala Gly Phe Ile Pro Pro Val
 115 120 125

Glu Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met Ser Ser Leu
 130 135 140

Tyr Gly Ser Asp Ala Ile Gly Gly Val Ile Asn Ile Ile Thr Lys Pro
 145 150 155 160

Val Asn Asn Gln Thr Trp Asp Gly Val Leu Gly Leu Gly Gly Ile Ile
 165 170 175

Gln Glu His Gly Lys Phe Gly Asn Ser Thr Thr Asn Asp Phe Tyr Leu
 180 185 190

Ser Gly Pro Leu Ile Lys Asp Lys Leu Gly Leu Gln Leu Tyr Gly Gly
 195 200 205

Met Asn Tyr Arg Lys Glu Asp Ser Ile Ser Gln Gly Thr Pro Ala Lys
 210 215 220

Asp Asn Lys Asn Ile Thr Ala Thr Leu Gln Phe Thr Pro Thr Glu Ser
 225 230 235 240

Gln Lys Phe Val Phe Glu Tyr Gly Lys Asn Asn Gln Val His Thr Leu
 245 250 255

Thr Pro Gly Glu Ser Leu Asp Ala Trp Thr Met Arg Gly Asn Leu Lys
 260 265 270

Gln Pro Asn Ser Lys Arg Glu Thr His Asn Ser Arg Ser His Trp Val
 275 280 285

Ala Ala Trp Asn Ala Gln Gly Glu Ile Leu His Pro Glu Ile Ala Val
 290 295 300

Tyr Gln Glu Lys Val Ile Arg Glu Val Lys Ser Gly Lys Lys Asp Lys
 305 310 315 320

Tyr Asn His Trp Asp Leu Asn Tyr Glu Ser Arg Lys Pro Glu Ile Thr
 325 330 335

Asn Thr Ile Ile Asp Ala Lys Val Thr Ala Phe Leu Pro Glu Asn Val
 340 345 350

Leu Thr Ile Gly Gly Gln Phe Gln His Ala Glu Leu Arg Asp Asp Ser
 355 360 365

Ala Thr Gly Lys Lys Thr Thr Glu Thr Gln Ser Val Ser Ile Lys Gln
 370 375 380

Lys Ala Val Phe Ile Glu Asn Glu Tyr Ala Ala Thr Asp Ser Leu Ala
 385 390 395 400

Leu Thr Gly Gly Leu Arg Leu Asp Asn His Glu Ile Tyr Gly Ser Tyr
 405 410 415

Trp Asn Pro Arg Leu Tyr Ala Val Tyr Asn Leu Thr Asp Asn Leu Thr
 420 425 430

Leu Lys Gly Gly Ile Ala Lys Ala Phe Arg Ala Pro Ser Ile Arg Glu
 435 440 445

Val Ser Pro Gly Phe Gly Thr Leu Thr Gln Gly Gly Ala Ser Ile Met
 450 455 460

Tyr Gly Asn Arg Asp Leu Lys Pro Glu Thr Ser Val Thr Glu Glu Ile
 465 470 475 480

Gly Ile Ile Tyr Ser Asn Asp Ser Gly Phe Ser Ala Ser Ala Thr Leu
 485 490 495

96

Phe Asn Thr Asp Phe Lys Asn Lys Leu Thr Ser Tyr Asp Ile Gly Thr
 500 505 510

Lys Asp Pro Val Thr Gly Leu Asn Thr Phe Ile Tyr Asp Asn Val Gly
 515 520 525

Glu Ala Asn Ile Arg Gly Val Glu Leu Ala Thr Gln Ile Pro Val Tyr
 530 535 540

Asp Lys Trp His Val Ser Ala Asn Tyr Thr Phe Thr Asp Ser Arg Arg
 545 550 555 560

Lys Ser Asp Asp Glu Ser Leu Asn Gly Lys Ser Leu Lys Gly Glu Pro
 565 570 575

Leu Glu Arg Thr Pro Arg His Ala Ala Asn Ala Lys Leu Glu Trp Asp
 580 585 590

Tyr Thr Gln Asp Ile Thr Phe Tyr Ser Ser Leu Asn Tyr Thr Gly Lys
 595 600 605

Gln Ile Trp Ala Ala Gln Arg Asn Gly Ala Lys Val Pro Arg Val Arg
 610 615 620

Asn Gly Phe Thr Ser Met Asp Ile Gly Leu Asn Tyr Gln Ile Leu Pro
 625 630 635 640

Asp Thr Leu Ile Asn Phe Ala Val Leu Asn Val Thr Asp Arg Lys Ser
 645 650 655

Glu Asp Ile Asp Thr Ile Asp Gly Asn Trp Gln Val Asp Glu Gly Arg
 660 665 670

Arg Tyr Trp Ala Asn Val Arg Val Ser Phe
 675 680

<210> 41
 <211> 164
 <212> PRT
 <213> Escherichia coli
 <400> 41

Met Gly Phe Arg Lys Thr Ile Ile Thr Ser Val Gly Leu Ile Phe Ile
 1 5 10 15

Ser Phe Ser Phe Val Ala Lys Cys Ser Gln Leu Lys Asn Leu Asn Asn
 20 25 30

Tyr Ser Val Met Leu Cys Gly Lys Val Ser Asn Asn Ile Leu Asp Asp
 35 40 45

Ile Gly Gly Tyr Lys Glu Arg Asn Ile Leu Met Leu Arg Ala Ile Lys
 50 55 60

Lys Ile Ile Ile Met Thr Ile Val Asn Ile Ile Phe Phe Tyr Ser Phe
 65 70 75 80

Gln Ser Thr Ala Asp Glu Met Val Leu Ile Lys Lys Tyr Gly Phe Gly
 85 90 95

Leu Glu Arg Asp Ile Lys Gly Arg Pro Leu Ile Tyr Pro Ile Glu Asn
 100 105 110

Tyr Asp Glu Cys Lys Lys Lys Cys Asn His Met Asn Tyr Ile Ala Asp
 115 120 125

Val Asn Ala Gln Leu Ala Met Ser Lys Lys Asn Asn Arg Ile Phe Ala
 130 135 140

Asn Ile Thr Phe Thr Asn Asn Ser Ser Thr Thr Tyr Phe Phe Leu Asn
 145 150 155 160

Ile Ile Tyr Leu

<210> 42

<211> 218

<212> PRT

<213> Escherichia coli

<400> 42

Met Asn Gln Ile Lys Asp Asn Lys Val Ile Met Lys Ile Lys Asn Leu
 1 5 10 15

Ile Ser Val Ile Leu Leu Ser Gly Gly Ile Met Gly Thr Gly Leu Tyr
 20 25 30

Ser Ser Asp Asn His Gln Lys Ile Arg Ser Arg Phe Asn Ile Gln Glu
 35 40 45

Ser Tyr Cys Ala Ile Lys Thr Asn Gly Val Leu Gly Phe Ser Asn Arg
50 55 60

Lys Asp Val Leu Arg Glu Asn Gly Asp Ser Thr Gly Thr Thr Ser Ser
65 70 75 80

Ser Thr Asn Ala Met Met Leu Met Glu Asn Gly Glu Asn Glu Ile Ser
85 90 95

Leu Glu Ile Gly Ala Leu Arg Trp Phe Ser Asp Lys Pro Ala Ser Thr
100 105 110

Glu Glu Arg Gly His Phe Ser Gln Lys Ala Gly Cys Ser Leu Asp Leu
115 120 125

Val Arg Phe Val Lys Gln Glu Glu Thr Ile Leu Ser Ser Ile Lys Val
130 135 140

Thr Ile Asn Gln Gln Gly Ile Pro Glu Ala Gln Pro Asp Ser Met His
145 150 155 160

Pro Val Ile Arg Lys Glu Ile Leu Ala Glu Gln Ala Glu Pro Gly Phe
165 170 175

Ile Asp Pro Asp Tyr Phe Asn Glu Thr Tyr Phe Pro Lys Gly Met Lys
180 185 190

Val Tyr Gln Phe Thr Gln Lys Val Ser Val Ala Gly Leu Pro Asp Gly
195 200 205

Pro Gly Arg Ser Thr Pro Phe Thr Gly Ala
210 215

<210> 43
<211> 2732
<212> PRT
<213> Escherichia coli
<400> 43

Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu
1 5 10 15

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala

20	25	30
Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly		
35	40	45
Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His		
50	55	60
Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn		
65	70	75
		80
Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln		
	85	90
		95
Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn		
	100	105
		110
Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val		
	115	120
		125
Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr		
	130	135
		140
Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr		
145	150	155
		160
Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val		
	165	170
		175
Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg		
	180	185
		190
Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala		
	195	200
		205
Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr		
	210	215
		220
Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys		
225	230	235
		240
Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile		
	245	250
		255

100

His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu
 260 265 270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr
 275 280 285

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly
 290 295 300

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser
 305 310 315 320

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys
 325 330 335

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys
 340 345 350

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln
 355 360 365

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala
 370 375 380

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu
 385 390 395 400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys
 405 410 415

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val
 420 425 430

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly
 435 440 445

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr
 450 455 460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser
 465 470 475 480

101

Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Thr Met His Leu Val Leu
 485 490 495

Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys Gly
 500 505 510

Leu Thr Val Ser Ala Thr Ser Ser Gly Lys Lys Ser Val Thr His Ser
 515 520 525

Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu Asp Gly Glu
 530 535 540

Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys Leu Ser Thr
 545 550 555 560

Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser Ile Asn Ala
 565 570 575

Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln Thr Met Val
 580 585 590

Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser Ser Ala Pro
 595 600 605

Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly Val Leu Val
 610 615 620

Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn Ser Gly Leu
 625 630 635 640

Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg Leu Asp Asn
 645 650 655

Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr Leu Asp Ile
 660 665 670

Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn Gly Leu Met
 675 680 685

Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile Ala Asp Thr
 690 695 700

102

Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu Leu Gln Gly
 705 710 715 720

Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln Gly Ser His
 725 730 735

Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly Lys Thr Leu
 740 745 750

Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val Gln Ala Asp
 755 760 765

Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn Leu Thr Ala
 770 775 780

Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met Ser Gln Gly
 785 790 795 800

Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly Ser Leu Leu
 805 810 815

Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp Asn Arg Gly
 820 825 830

Thr Val Gln Gly Asn His Val Thr Ile Arg Gln Asn Ser Val Thr Asn
 835 840 845

Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala Ala Arg Met
 850 855 860

Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser Leu Leu Thr
 865 870 875 880

Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser Ser Gly His
 885 890 895

Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu Ala Asn Ser
 900 905 910

Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu Thr Gly Glu
 915 920 925

Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly Glu Met Ala

930 935 940
 Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile Ala Lys Asn
 945 950 955 960
 Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp Ile Thr Gly
 965 970 975
 Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn Asn Gln Ala
 980 985 990
 Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu Lys Ala Asp Ser
 995 1000 1005
 Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val Thr Thr Ile Thr
 1010 1015 1020
 Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln Gly Glu Thr Leu
 1025 1030 1035
 Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg Ser Gly Gly Val
 1040 1045 1050
 Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr Ala Thr Leu Ser
 1055 1060 1065
 Asn Gln Ser Thr Ile Gln Gly Gly Gly Gly Val Ser Leu Asn Ala
 1070 1075 1080
 Thr Asp Arg Leu Gln Asn Asp Gly Lys Ile Leu Ser Gly Ser Asn
 1085 1090 1095
 Leu Thr Leu Thr Ala Gln Val Leu Ala Asn Thr Gly Ser Gly Leu
 1100 1105 1110
 Val Gln Ala Ala Thr Leu Leu Leu Asp Val Val Asn Thr Val Asn
 1115 1120 1125
 Gly Gly Arg Val Leu Ala Thr Gly Ser Asp Val Lys Gly Thr Thr
 1130 1135 1140
 Leu Asn Asn Thr Gly Thr Leu Gln Gly Ala Thr Leu Val Asn Tyr
 1145 1150 1155

His Thr Phe Ser Ser Gly Thr Leu Leu Gly Thr Ser Gly Leu Gly
 1160 1165 1170
 Val Lys Gly Ser Ser Leu Leu Gln Asn Gly Thr Gly Arg Leu Tyr
 1175 1180 1185
 Ser Ala Gly Asn Leu Leu Leu Asp Ala Gln Asp Phe Ser Gly Gln
 1190 1195 1200
 Gly Gln Val Val Ala Thr Gly Asp Val Thr Leu Lys Leu Ile Ala
 1205 1210 1215
 Ala Leu Thr Asn His Gly Thr Leu Ala Ala Gly Lys Thr Leu Ser
 1220 1225 1230
 Val Thr Ser Gln Asn Ala Ile Thr Asn Gly Gly Val Met Gln Gly
 1235 1240 1245
 Asp Ala Met Val Leu Gly Ala Gly Glu Ala Phe Thr Asn Asn Gly
 1250 1255 1260
 Leu Thr Ala Gly Lys Gly Asn Ser Val Phe Ser Ala Gln Arg Leu
 1265 1270 1275
 Phe Leu Asn Ala Pro Gly Ser Leu Gln Gly Gly Gly Asp Val Ser
 1280 1285 1290
 Leu Asn Ser Arg Ser Asp Ile Thr Ile Ser Gly Phe Thr Gly Thr
 1295 1300 1305
 Ala Gly Ser Leu Thr Met Asn Val Ala Gly Thr Leu Leu Asn Ser
 1310 1315 1320
 Ala Leu Ile Tyr Ala Gly Asn Asn Leu Lys Leu Phe Thr Asp Arg
 1325 1330 1335
 Leu His Asn Gln His Gly Asp Ile Leu Ala Gly Asn Ser Leu Trp
 1340 1345 1350
 Val Gln Lys Asp Ala Ser Gly Gly Ala Asn Thr Glu Ile Ile Asn
 1355 1360 1365

Asn Ser Gly Asn Ile Glu Thr His Gln Gly Asp Ile Val Val Arg	
1370	1375 1380
Thr Gly His Leu Leu Asn Gln Arg Glu Gly Phe Ser Ala Thr Thr	
1385	1390 1395
Thr Thr Arg Thr Asn Pro Ser Ser Ile Gln Gly Met Gly Asn Ala	
1400	1405 1410
Leu Val Asp Ile Pro Leu Ser Leu Leu Pro Asp Gly Ser Tyr Gly	
1415	1420 1425
Tyr Phe Thr Arg Glu Val Glu Asn Gln His Gly Thr Pro Cys Asn	
1430	1435 1440
Gly His Gly Ala Cys Asn Ile Thr Met Asp Thr Leu Tyr Tyr Tyr	
1445	1450 1455
Ala Pro Phe Ala Asp Ser Ala Thr Gln Arg Phe Leu Ser Ser Gln	
1460	1465 1470
Asn Ile Thr Thr Val Thr Gly Ala Asp Asn Pro Ala Gly Arg Ile	
1475	1480 1485
Ala Ser Gly Arg Asn Leu Ser Ala Glu Ala Glu Arg Leu Glu Asn	
1490	1495 1500
Arg Ala Ser Phe Ile Leu Ala Asn Gly Asp Ile Ala Leu Ser Gly	
1505	1510 1515
Arg Glu Leu Ser Asn Gln Ser Trp Gln Thr Gly Thr Glu Asn Glu	
1520	1525 1530
Tyr Leu Val Tyr Arg Tyr Asp Pro Lys Thr Phe Tyr Gly Ser Tyr	
1535	1540 1545
Ala Thr Gly Ser Leu Asp Lys Leu Pro Leu Leu Ser Pro Glu Phe	
1550	1555 1560
Glu Asn Asn Thr Ile Arg Phe Ser Leu Asp Gly Arg Glu Lys Asp	
1565	1570 1575

106

Tyr	Thr	Pro	Gly	Lys	Thr	Tyr	Tyr	Ser	Val	Ile	Gln	Ala	Gly	Gly
1580						1585					1590			
Asp	Val	Lys	Thr	Arg	Phe	Thr	Ser	Ser	Ile	Asn	Asn	Gly	Thr	Thr
1595						1600					1605			
Thr	Ala	His	Ala	Gly	Ser	Val	Ser	Pro	Val	Val	Ser	Ala	Pro	Val
1610						1615					1620			
Leu	Asn	Thr	Leu	Ser	Gln	Gln	Thr	Gly	Gly	Asp	Ser	Leu	Thr	Gln
1625						1630					1635			
Thr	Ala	Leu	Gln	Gln	Tyr	Glu	Pro	Val	Val	Val	Gly	Ser	Pro	Gln
1640						1645					1650			
Trp	His	Asp	Glu	Leu	Ala	Gly	Ala	Leu	Lys	Asn	Ile	Ala	Gly	Gly
1655						1660					1665			
Ser	Pro	Leu	Thr	Gly	Gln	Thr	Gly	Ile	Ser	Asp	Asp	Trp	Pro	Leu
1670						1675					1680			
Pro	Ser	Gly	Asn	Asn	Gly	Tyr	Leu	Val	Pro	Ser	Thr	Asp	Pro	Asp
1685						1690					1695			
Ser	Pro	Tyr	Leu	Ile	Thr	Val	Asn	Pro	Lys	Leu	Asp	Gly	Leu	Gly
1700						1705					1710			
Gln	Val	Asp	Ser	His	Leu	Phe	Ala	Gly	Leu	Tyr	Glu	Leu	Leu	Gly
1715						1720					1725			
Ala	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Glu	Thr	Ala	Pro	Ser	Tyr	Thr
1730						1735					1740			
Asp	Glu	Lys	Gln	Phe	Leu	Gly	Ser	Ser	Tyr	Phe	Leu	Asp	Arg	Leu
1745						1750					1755			
Gly	Leu	Lys	Pro	Glu	Lys	Asp	Tyr	Arg	Phe	Leu	Gly	Asp	Ala	Val
1760						1765					1770			
Phe	Asp	Thr	Arg	Tyr	Val	Ser	Asn	Ala	Val	Leu	Ser	Arg	Thr	Gly
1775						1780					1785			
Ser	Arg	Tyr	Leu	Asn	Gly	Leu	Gly	Ser	Asp	Thr	Glu	Gln	Met	Arg

1790	1795	1800
Tyr Leu Met Asp Asn Ala Ala Arg Gln Gln Lys Gly Leu Gly Leu 1805 1810 1815		
Glu Phe Gly Val Ala Leu Thr Ala Glu Gln Ile Ala Gln Leu Asp 1820 1825 1830		
Gly Ser Ile Leu Trp Trp Glu Ser Val Thr Ile Asn Gly Gln Thr 1835 1840 1845		
Val Met Val Pro Lys Leu Tyr Leu Ser Pro Glu Asp Ile Thr Leu 1850 1855 1860		
His Asn Gly Ser Val Ile Ser Gly Asn Asn Val Gln Leu Ala Gly 1865 1870 1875		
Gly Asn Ile Thr Asn Ser Gly Gly Ser Ile Asn Ala Gln Asn Asp 1880 1885 1890		
Leu Ser Leu Asp Ser Ser Gly Tyr Ile Asp Asn Leu Asn Ala Gly 1895 1900 1905		
Leu Ile Ser Ala Gly Gly Ser Leu Asp Leu Ser Ala Ile Gly Asp 1910 1915 1920		
Ile Ser Asn Ile Ser Ser Val Ile Ser Gly Lys Thr Val Gln Leu 1925 1930 1935		
Glu Ser Val Ser Gly Asn Ile Ser Asn Ile Thr Arg Arg Gln Gln 1940 1945 1950		
Trp Asn Ala Gly Ser Asp Ser Gln Tyr Gly Gly Val His Leu Ser 1955 1960 1965		
Gly Thr Asp Thr Gly Pro Val Ala Thr Ile Lys Gly Thr Asp Ser 1970 1975 1980		
Leu Ser Leu Asp Ala Gly Lys Asn Ile Asp Ile Thr Gly Ala Thr 1985 1990 1995		
Val Ser Ser Gly Gly Asp Leu Gly Met Ser Ala Gly Asn Asp Ile 2000 2005 2010		

Asn	Ile	Ala	Ala	Asn	Leu	Ile	Ser	Gly	Ser	Lys	Ser	Gln	Ser	Gly
2015						2020					2025			
Phe	Trp	His	Thr	Asp	Asp	Asn	Ser	Ser	Ser	Ser	Thr	Thr	Ser	Gln
2030						2035					2040			
Gly	Ser	Ser	Ile	Ser	Ala	Gly	Gly	Asn	Leu	Ala	Met	Ala	Ala	Gly
2045						2050					2055			
His	Asn	Leu	Asp	Val	Thr	Ala	Ser	Ser	Val	Ser	Ala	Gly	His	Ser
2060						2065					2070			
Ala	Leu	Leu	Ser	Cys	Arg	Ser	Arg	Pro	Ser	Leu	Glu	Cys	Ser	Gln
2075						2080					2085			
Gly	Lys	Ala	Lys	Thr	Ser	Arg	Asn	Gly	Arg	Ser	Glu	Ser	His	Glu
2090						2095					2100			
Ser	His	Ala	Ala	Val	Ser	Thr	Val	Thr	Ala	Gly	Asp	Asn	Phe	Leu
2105						2110					2115			
Leu	Val	Ala	Gly	Arg	Asp	Ile	Ala	Ser	Gln	Ala	Ala	Gly	Met	Ala
2120						2125					2130			
Ala	Glu	Asn	Asn	Val	Val	Ile	Arg	Gly	Gly	Arg	Asp	Val	Asn	Leu
2135						2140					2145			
Val	Ala	Glu	Ser	Ala	Gly	Ala	Gly	Asp	Ser	Tyr	Thr	Ser	Lys	Lys
2150						2155					2160			
Lys	Lys	Glu	Ile	Asn	Glu	Thr	Val	Arg	Gln	Gln	Gly	Thr	Glu	Ile
2165						2170					2175			
Ala	Ser	Gly	Gly	Asp	Thr	Thr	Val	Asn	Ala	Gly	Arg	Asp	Ile	Thr
2180						2185					2190			
Ala	Val	Ala	Ser	Ser	Val	Thr	Ala	Thr	Gly	Asn	Ile	Ser	Val	Asn
2195						2200					2205			
Ala	Gly	Arg	Asp	Val	Ala	Leu	Thr	Thr	Ala	Thr	Glu	Ser	Asp	Tyr
2210						2215					2220			

His Tyr Leu Glu Thr Lys Lys Lys Ser Gly Gly Phe Leu Ser Lys
 2225 2230 2235
 Lys Thr Thr Arg Thr Ile Ser Glu Asp Ser Ala Thr Arg Glu Ala
 2240 2245 2250
 Gly Ser Leu Leu Ser Gly Asn Arg Val Thr Val Asn Ala Gly Asp
 2255 2260 2265
 Asn Leu Thr Val Glu Gly Ser Asp Val Val Ala Asp Arg Asp Val
 2270 2275 2280
 Ser Leu Ala Ala Gly Asn His Val Asp Val Leu Ala Ala Thr Ser
 2285 2290 2295
 Thr Asp Thr Ser Trp Arg Phe Lys Glu Thr Lys Lys Ser Gly Leu
 2300 2305 2310
 Met Gly Thr Gly Gly Ile Gly Phe Thr Ile Gly Ser Ser Lys Thr
 2315 2320 2325
 Thr His Asp Arg Arg Glu Ala Gly Thr Thr Gln Ser Gln Ser Ala
 2330 2335 2340
 Ser Thr Ile Gly Ser Thr Ala Gly Asn Val Ser Ile Thr Ala Gly
 2345 2350 2355
 Lys Gln Ala His Ile Ser Gly Ser Asp Val Ile Ala Asn Arg Asp
 2360 2365 2370
 Ile Ser Ile Thr Gly Asp Ser Val Val Val Asp Pro Gly His Asp
 2375 2380 2385
 Arg Arg Thr Val Asp Glu Lys Phe Glu Gln Lys Lys Ser Gly Leu
 2390 2395 2400
 Thr Val Ala Leu Ser Gly Thr Val Gly Ser Ala Ile Asn Asn Ala
 2405 2410 2415
 Val Thr Ser Ala Gln Glu Thr Lys Glu Ser Ser Asp Ser Arg Leu
 2420 2425 2430

110

Lys Ala	Leu Gln Ala Thr	Lys Thr Ala Leu Ser	Gly Val Gln Ala
2435		2440	2445
Gly Gln	Ala Ala Thr Met	Ala Ser Ala Thr Gly	Asp Pro Asn Ala
2450		2455	2460
Gly Val	Ser Leu Ser Leu Thr	Thr Gln Lys Ser	Lys Ser Gln Gln
2465		2470	2475
His Ser	Glu Ser Asp Thr	Val Ser Gly Ser Thr	Leu Asn Ala Gly
2480		2485	2490
Asn Asn	Leu Ser Val Val	Ala Thr Gly Lys Asn	Arg Gly Asp Asn
2495		2500	2505
Arg Gly	Asp Ile Val Ile	Ala Gly Ser Gln Leu	Lys Ala Gly Gly
2510		2515	2520
Asn Thr	Ser Leu Asp Ala	Ala Asn Asp Ile Leu	Leu Ser Gly Ala
2525		2530	2535
Ala Asn	Thr Gln Lys Thr	Thr Gly Arg Asn Ser	Ser Ser Gly Gly
2540		2545	2550
Gly Val	Gly Val Ser Ile	Gly Ala Gly Lys Gly	Ala Gly Ile Ser
2555		2560	2565
Ala Phe	Ala Ser Val Asn	Ala Ala Lys Gly Arg	Glu Lys Gly Asn
2570		2575	2580
Gly Thr	Thr Thr Asp Lys	Thr Val Thr Ile Asn	Ser Gly Arg Asp
2585		2590	2595
Thr Val	Leu Asn Gly Ala	Gln Val Asn Gly Asn	Arg Ile Ile Ala
2600		2605	2610
Asp Val	Gly His Asp Leu	Leu Ile Ser Ser Gln	Gln Asp Thr Ser
2615		2620	2625
Lys Tyr	Asp Ser Lys Gln	Thr Ser Val Ala Ala	Gly Gly Ser Phe
2630		2635	2640
Thr Phe	Gly Ser Met Thr	Gly Ser Gly Tyr Ile	Ala Ala Ser Arg

111

2645

2650

2655

Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr Gly
 2660 2665 2670

Met Phe Ala Arg Val Met Val Ala Ser Thr Ser Gln Trp Val Asn
 2675 2680 2685

Ile Pro Asn Trp Met Val Arg Ser Leu Pro His Cys His Thr Gly
 2690 2695 2700

Glu Lys Pro Pro Gly Tyr Arg Thr Leu Gly Leu Val Thr Leu Gln
 2705 2710 2715

Arg Ser Gly Ile Ile Lys Ser Ser His Arg Trp Asn Gln Ser
 2720 2725 2730

<210> 44

<211> 321

<212> PRT

<213> Escherichia coli

<400> 44

Met Met Leu Lys Lys Thr Ile Phe Ile Leu Thr Leu Phe Ser Gly Asn
 1 5 10 15

Val Ile Ala Ala Thr Val Glu Leu Gly Phe Glu Asn Glu Gln Tyr Asn
 20 25 30

Tyr Ala Tyr Arg Ser Ala Asp Val Phe Met Pro Tyr Ile Lys Ser Asn
 35 40 45

Phe Asn Pro Val Thr Asp Ser Ala Leu Asn Val Ser Leu Thr Tyr Met
 50 55 60

Tyr Gln Asp Gln Tyr Gly Lys Lys His Lys Lys Thr Ser Glu Asp Arg
 65 70 75 80

Phe Lys Thr Asn Arg Asp Arg Ile Glu Leu Tyr Leu Lys Gly Tyr Thr
 85 90 95

Leu Asn Arg Gly Ala Tyr Ser Phe Ser Pro Ser Ala Gly Phe Arg Tyr
 100 105 110

112

Glu Ser Trp Asp Val Asn Tyr Asp Asn Pro Lys Lys Gln Asp Lys Trp
 115 120 125

Lys Leu Glu Leu Arg Phe Tyr Pro Asn Met Thr Tyr Lys Leu Asn Asp
 130 135 140

Gln Leu Ser Leu Tyr Met Asn Gly Phe Val Ala Pro Val Phe Phe Lys
 145 150 155 160

Thr Gln Gln Glu Ser Arg Lys Asp Asn Asn Tyr Val Lys Gly Lys Leu
 165 170 175

Gly Ala Lys Arg Tyr Asn Asn Asp Tyr Tyr Gln Glu Leu Gln Ile Leu
 180 185 190

Gly Val Arg Tyr Lys Phe Asn Asn Asp Asn Thr Leu Trp Ala Ser Val
 195 200 205

Tyr Asn Glu Arg Lys Tyr Asn Gln His Ser Ser Lys Tyr Asp Arg Trp
 210 215 220

Gln Leu Arg Gly Gly Tyr Asp Phe Lys Val Thr Glu Glu Phe Val Leu
 225 230 235 240

Ser Pro Phe Ile Arg Tyr Asp Leu Ser Tyr Arg Glu Lys Asn Leu Glu
 245 250 255

Ser Thr Ser Asn Asn Gly Leu Ser Lys Asn Asn Lys Glu Ile Arg Thr
 260 265 270

Gly Ala Ser Phe Ser Tyr Lys Ile Ile Pro Ser Val Lys Leu Val Gly
 275 280 285

Glu Ile Tyr Arg Gln Thr Thr Asn Ile Glu Asn Tyr Tyr Gly Glu His
 290 295 300

Ser Glu Asp Lys Asn Arg Met Phe Tyr Lys Leu Gly Ile Asn Lys Thr
 305 310 315 320

Phe

<210> 45

113

<211> 587
 <212> PRT
 <213> Escherichia coli
 <400> 45

Met Gln His Arg Gln Lys Asn Ile Leu Thr Lys Thr Ser Leu Leu Ser
 1 5 10 15

Arg Ala Leu Ser Val Pro Cys Cys Asp Met Phe Arg Arg Gly Ser Pro
 20 25 30

Trp Ile Cys Tyr Leu Ser Leu Ser Val Phe Ser Gly Cys Phe Ile Pro
 35 40 45

Ala Phe Ser Ser Pro Ala Ala Met Leu Ser Pro Gly Asp Arg Ser Ala
 50 55 60

Ile Gln Gln Gln Gln Gln Gln Leu Leu Asp Glu Asn Gln Arg Gln Arg
 65 70 75 80

Asp Ala Leu Glu Arg Pro Leu Thr Ile Thr Pro Ser Pro Glu Thr Ser
 85 90 95

Ala Gly Thr Glu Gly Pro Cys Phe Thr Val Ser Ser Ile Val Val Ser
 100 105 110

Gly Ala Thr Arg Leu Thr Ser Ala Glu Thr Asp Arg Leu Val Pro Trp
 115 120 125

Val Asn Gln Cys Leu Asn Ile Thr Gly Leu Thr Ala Val Thr Asp Ala
 130 135 140

Val Thr Asp Gly Tyr Ile Arg Arg Gly Tyr Ile Thr Ser Arg Ala Phe
 145 150 155 160

Leu Thr Glu Gln Asp Leu Ser Gly Gly Val Leu His Ile Thr Val Met
 165 170 175

Glu Gly Arg Leu Gln Gln Ile Arg Ala Glu Gly Ala Asp Leu Pro Ala
 180 185 190

Arg Thr Leu Lys Met Val Phe Pro Gly Met Glu Gly Lys Val Leu Asn
 195 200 205

114

Leu Arg Asp Ile Glu Gln Gly Met Glu Gln Ile Asn Arg Leu Arg Thr
 210 215 220

Glu Pro Val Gln Ile Glu Ile Ser Pro Gly Asp Arg Glu Gly Trp Ser
 225 230 235 240

Val Val Thr Leu Thr Ala Leu Pro Glu Trp Pro Val Thr Gly Ser Val
 245 250 255

Gly Ile Asp Asn Ser Gly Gln Lys Ser Thr Gly Thr Gly Gln Leu Asn
 260 265 270

Gly Val Leu Ser Phe Asn Asn Pro Leu Gly Leu Ala Asp Asn Trp Phe
 275 280 285

Val Ser Gly Gly Arg Ser Ser Asp Phe Ser Val Ser His Asp Ala Arg
 290 295 300

Asn Phe Ala Ala Gly Val Ser Leu Pro Tyr Gly Tyr Thr Leu Val Asp
 305 310 315 320

Tyr Thr Tyr Ser Trp Ser Asp Tyr Leu Ser Thr Ile Asp Asn Arg Gly
 325 330 335

Trp Arg Trp Arg Ser Thr Gly Asp Leu Gln Thr His Arg Leu Gly Leu
 340 345 350

Ser His Val Leu Phe Arg Asn Gly Asp Met Lys Thr Ala Leu Thr Gly
 355 360 365

Gly Leu Gln His Arg Ile Ile His Asn Tyr Leu Asp Asp Val Leu Leu
 370 375 380

Gln Gly Ser Ser Arg Lys Leu Thr Ser Phe Ser Val Gly Leu Asn His
 385 390 395 400

Thr His Lys Phe Leu Gly Gly Val Gly Thr Leu Asn Pro Val Phe Thr
 405 410 415

Arg Gly Met Pro Trp Phe Gly Ala Glu Ser Asp His Gly Lys Arg Gly
 420 425 430

Asp Leu Pro Val Asn Gln Phe Arg Lys Trp Ser Val Ser Ala Ser Phe

115

435

440

445

Gln Arg Pro Val Thr Asp Arg Val Trp Trp Leu Thr Ser Ala Tyr Ala
 450 455 460

Gln Trp Ser Pro Asp Arg Leu His Gly Val Glu Gln Leu Ser Leu Gly
 465 470 475 480

Gly Glu Ser Ser Val Arg Gly Phe Lys Asp Gln Tyr Ile Ser Gly Asn
 485 490 495

Asn Gly Gly Tyr Leu Arg Asn Glu Leu Ser Trp Ser Leu Phe Ser Leu
 500 505 510

Pro Tyr Val Gly Thr Val Arg Ala Val Ala Ala Leu Asp Gly Gly Trp
 515 520 525

Leu His Ser Asp Ser Asp Asp Pro Tyr Ser Ser Gly Thr Leu Trp Gly
 530 535 540

Ala Ala Ala Gly Leu Ser Thr Thr Ser Gly His Val Ser Gly Ser Phe
 545 550 555 560

Thr Ala Gly Leu Pro Leu Val Tyr Pro Asp Trp Leu Ala Pro Asp His
 565 570 575

Leu Thr Val Tyr Trp Arg Val Ala Val Ala Phe
 580 585

<210> 46

<211> 744

<212> PRT

<213> Escherichia coli

<400> 46

Met Asn Lys His Thr Leu Leu Leu Thr Val Leu Phe Leu Asn Leu Ile
 1 5 10 15

Cys Thr Pro Val Phe Ala Gln Asn Trp Gln Val Ala Thr Phe Gly Gln
 20 25 30

Ser Thr Asp Leu Asn Phe Ser Ser Leu Ile Asp Ser Ala Lys Ile Gly
 35 40 45

116

Arg Asn Asn Ala Trp Leu Ala Gly Asn Asn Asn Phe Leu Glu Ala Gly
 50 55 60

Lys Phe Tyr Thr Leu Pro Thr Asp Phe Phe Ile Glu Ser Arg Gly Gly
 65 70 75 80

Lys Ile Ala Asn Ser His Asp Gly Met Thr Val Phe Tyr Thr Ile Val
 85 90 95

Pro Val Thr Gln Thr Phe Arg Leu Glu Ala Asp Leu Thr Leu Glu Gln
 100 105 110

Ile Gly Pro Glu Val Asn Gly Lys Ser Pro Ala Gly Gln Glu Gly Ala
 115 120 125

Gly Leu Phe Val Arg Asp Ile Ile Gly Pro Gln Arg Gln Glu Pro Gln
 130 135 140

Ser Ala Gly Thr Glu Glu Tyr Pro Gln Ala Ser Asn Ile Leu Met Asn
 145 150 155 160

Ala Phe Ile Thr Gln Asn Lys Lys Asn Asp Asn Leu Val Gln Ile Thr
 165 170 175

Ser Ile Val Arg Glu Gly Val Ile Lys Thr Trp Gly Asn Glu Gly Ile
 180 185 190

Thr Ile Lys Lys Gln Pro Ile Ile Glu Asn Ile Asn Phe Thr Gln Lys
 195 200 205

Arg Asn Ile His Met Thr Ile Glu Arg Leu Pro Glu Lys Phe Ile Leu
 210 215 220

Thr Ala Phe Asp Thr Asp Arg Lys Glu Asn Gln Ser Trp Gln Phe Ser
 225 230 235 240

Asp Tyr Ser Gly Phe Met Asn Gln Leu Asp Asn Asn Ser Leu Ala Ile
 245 250 255

Gly Phe Phe Ala Ala Arg Asn Ala Lys Leu Arg Val Lys Asn Ala Ser
 260 265 270

Phe Lys Pro Gly Lys Pro Leu Val Asp Tyr Lys Gln Leu Thr Ser Arg

117

275

280

285

Gln Phe Ser Arg Val Arg His Lys Ala Pro Glu Leu Phe Leu Ala Ser
 290 295 300

Pro Gln Ser Val Val Arg Asn Ser Thr Thr Leu Gln Phe Leu Ala Asn
 305 310 315 320

Gln Ala Gly Ile Val Ser Ile Asp Asn Asp Lys Gln Thr Lys Gln Val
 325 330 335

Gln Ala Gly Glu Leu Val Gln Phe Pro Val Thr Leu Gln Lys Lys His
 340 345 350

Asn Asp Phe Thr Val Asn Phe Asn Val Asp Gly Asn Ile Ser Lys Lys
 355 360 365

Ala Ile Arg Ile Glu Gln Val Lys Ser Asn Leu Thr Asp Pro Tyr Glu
 370 375 380

Ile Tyr Val Cys Ser Asp Cys Arg Gln Gly Ala Arg Gly Ser Lys Asn
 385 390 395 400

Asp Pro Val Asp Leu Gln Thr Ala Val Lys Phe Val Ala Pro Gly Gly
 405 410 415

Asn Ile Tyr Leu Asn Asp Gly Gln Tyr His Gly Ile Thr Leu Asp Arg
 420 425 430

Glu Leu Ser Gly Ile Pro Gly Lys Tyr Lys Thr Ile Ser Ala Ile Asn
 435 440 445

Pro His Lys Ala Ile Phe Ile Asn Lys Thr Phe Asn Leu Asp Ala Ser
 450 455 460

Tyr Trp His Leu Lys Ser Val Val Phe Asp Gly Asn Val Asp Asn Gly
 465 470 475 480

Asn Asn Lys Pro Ala Tyr Leu Arg Ile Ala Gly Ser Tyr Asn Ile Ile
 485 490 495

Glu His Val Ile Ala Arg Asn Asn Asp Asp Thr Gly Ile Ser Ile Ser
 500 505 510

Ala Lys Asp Lys Asn Arg Phe Phe Trp Pro Ala His Asn Leu Val Leu
515 520 525

Asn Ser Asp Ser Tyr Asn Asn Leu Asp Leu Ser Gly Ile Asn Ala Asp
530 535 540

Gly Phe Ala Ala Lys Leu Gly Val Gly Pro Gly Asn Ile Phe Arg Gly
545 550 555 560

Cys Ile Ala His Asn Asn Ala Asp Asp Gly Trp Asp Leu Phe Asn Lys
565 570 575

Ile Glu Asp Gly Pro Asn Ala Ser Val Thr Ile Glu Asn Ser Val Ala
580 585 590

Tyr Glu Asn Gly Leu Pro Tyr Asn Lys Ala Asp Ile Leu Lys Gly Ser
595 600 605

Ile Gly Asn Gly Gly Glu Gly Gln Pro Ser Lys Ser Gln Val Ile Asn
610 615 620

Ser Ile Ala Ile Asn Asn Asn Met Asp Gly Phe Thr Asp Asn Phe Asn
625 630 635 640

Thr Gly Ser Leu Ile Val Arg Asn Asn Ile Ala Met Asn Asn Ala Arg
645 650 655

Tyr Asn Tyr Ile Leu Arg Thr Asn Pro Tyr Lys Phe Pro Ser Ser Ile
660 665 670

Leu Phe Asp Asn Asn Tyr Ser Ile Arg Asp Asp Trp Glu Asn Lys Ile
675 680 685

Lys Asp Phe Leu Gly Asp Thr Val Asn Ser Val Asn Tyr Lys Leu Leu
690 695 700

Val Ser His Glu Thr Gly Pro Val Gln Lys Asp Leu Phe Phe Thr Arg
705 710 715 720

Asp Asp Ser Gly Asn Ile Ile Tyr Pro Asp Phe Phe Leu Asn Ile Ile
725 730 735

119

Asn Lys Phe Asn Glx Thr Met Pro
740

<210> 47
<211> 136
<212> PRT
<213> Escherichia coli
<400> 47

Met Lys Thr Phe Ile Lys Thr Leu Leu Val Ala Val Thr Ile Leu Phe
1 5 10 15

Ser Val Phe Ala Thr Ala Lys Gln Val Lys Leu Pro Asn Asn Ile Lys
20 25 30

Tyr Val Asn Thr Thr Glu Ala Phe Ser Cys Thr Glu Ile Asp Gly Met
35 40 45

Asn Cys Gln Thr Lys Asn Pro Phe Asn Tyr Lys Asp Asn Ser Tyr Val
50 55 60

Phe Val Leu Glu Arg Gly Gly Ala Trp Cys Tyr Asp Tyr Thr Val Ser
65 70 75 80

Val Leu Asn Leu Lys Thr Gly Lys Ala Gln Met Leu Glu Tyr Lys Asp
85 90 95

Asn Gln Leu Cys Ser Gly Ser Asn Lys Pro Phe Phe Glu Ile Lys Asn
100 105 110

Gly Val Pro Thr Val Gly Val Ile Asp Thr Ser Gly Lys Pro Val Val
115 120 125

Val Ala Leu Asp Lys Leu Lys Thr
130 135

<210> 48
<211> 225
<212> PRT
<213> Escherichia coli
<400> 48

Met Gln Leu Pro Val Lys Leu Leu Met Ser Leu Ile Ser Leu Val Ser
1 5 10 15

120

Val Ile Ala Arg Ala Gly Lys Tyr Lys Asn Tyr Ile Arg Asp Glu Ile
 20 25 30

Lys Tyr Trp Arg Tyr Thr Ser Tyr Lys Gly Gly Glu Phe Pro Glu Gly
 35 40 45

Phe Thr Asp Glu Lys Phe Ser Ser Ala Ile Tyr Asn Gly Arg Ile Phe
 50 55 60

Thr Met Lys Arg Leu His Thr Leu Met Leu Phe Leu Ala Val Leu Phe
 65 70 75 80

Thr Gly Phe Asn Val Glu Ala Ala Ser Val Lys Gln Ala Leu Ser Cys
 85 90 95

Asp Pro Asn Ala Arg Ala Glu Gln Pro Gly Ala Cys Pro Thr Thr Tyr
 100 105 110

Glu Leu Tyr Glu Gly Asp Ala Ala Tyr Lys Ala Ala Leu Asp Lys Ala
 115 120 125

Leu Lys Pro Val Gly Leu Ser Gly Met Phe Gly Lys Gly Gly Tyr Met
 130 135 140

Asp Gly Pro Gly Gly Asn Val Thr Pro Val Thr Ile Asn Gly Thr Val
 145 150 155 160

Trp Leu Gln Gly Asp Gly Cys Lys Ala Asn Thr Cys Gly Trp Asp Phe
 165 170 175

Ile Val Thr Leu Tyr Asn Pro Lys Thr His Glu Val Val Gly Tyr Arg
 180 185 190

Tyr Phe Gly Leu Asp Asp Pro Ala Tyr Leu Val Trp Phe Gly Glu Ile
 195 200 205

Gly Val His Glu Phe Ala Tyr Leu Val Lys Asn Tyr Val Ala Ala Val
 210 215 220

Asn
 225

<210> 49

121

<211> 721
 <212> PRT
 <213> Escherichia coli
 <400> 49

Met Lys Thr Gln Ile Thr Phe Ala Ala Leu Leu Pro Ala Leu Ala Ser
 1 5 10 15

Phe Ile Pro Leu His Ala His Ala Ser Ser Thr Ser Glu Asp Glu Met
 20 25 30

Ile Val Thr Gly Asn Thr Ala Ala Asp Thr Thr Asp Ser Ala Ala Gly
 35 40 45

Ala Gly Phe Lys Thr Asn Asp Ile Asp Val Gly Pro Leu Gly Thr Lys
 50 55 60

Ser Trp Ile Glu Thr Pro Tyr Ser Ser Thr Thr Val Thr Lys Glu Met
 65 70 75 80

Ile Glu Asn Gln Gln Ala Gln Ser Val Ser Glu Met Leu Lys Tyr Ser
 85 90 95

Pro Ser Thr Gln Met Gln Ala Arg Gly Gly Met Asp Val Gly Arg Pro
 100 105 110

Gln Ser Arg Gly Met Gln Gly Ser Val Val Ala Asn Ser Arg Leu Asp
 115 120 125

Gly Leu Asn Ile Val Ser Thr Thr Ala Phe Pro Val Glu Met Leu Glu
 130 135 140

Arg Met Asp Val Leu Asn Ser Leu Thr Gly Ala Leu Tyr Gly Pro Ala
 145 150 155 160

Ser Pro Ala Gly Gln Phe Asn Phe Val Ala Lys Arg Pro Thr Glu Glu
 165 170 175

Thr Leu Arg Lys Val Thr Leu Gly Tyr Gln Ser Arg Ser Ala Phe Thr
 180 185 190

Gly His Ala Asp Leu Gly Gly His Phe Asp Glu Asn Lys Arg Phe Gly
 195 200 205

122

Tyr Arg Val Asn Leu Leu Asp Gln Glu Gly Glu Gly Asn Val Asp Asp
 210 215 220

Ser Thr Leu Arg Arg Lys Leu Val Ser Val Ala Leu Asp Trp Asn Ile
 225 230 235 240

Gln Pro Gly Thr Gln Leu Gln Leu Asp Ala Ser His Tyr Glu Phe Ile
 245 250 255

Gln Lys Gly Tyr Val Gly Ser Phe Asn Tyr Gly Pro Asn Val Lys Leu
 260 265 270

Pro Ser Ala Pro Asn Pro Lys Asp Lys Asn Leu Ala Leu Ser Thr Ala
 275 280 285

Gly Asn Asp Leu Thr Thr Asp Thr Ile Ser Thr Arg Leu Ile His Tyr
 290 295 300

Phe Asn Asp Asp Trp Ser Met Asn Ala Gly Val Gly Trp Gln Gln Ala
 305 310 315 320

Asp Arg Ala Met Arg Ser Val Ser Ser Lys Ile Leu Asn Asn Gln Gly
 325 330 335

Asp Ile Ser Arg Ser Met Lys Asp Ser Thr Ala Ala Gly Arg Phe Arg
 340 345 350

Val Leu Ser Asn Thr Ala Gly Leu Asn Gly His Ile Asp Thr Gly Ser
 355 360 365

Ile Gly His Asp Leu Ser Leu Ser Thr Thr Gly Tyr Val Trp Ser Leu
 370 375 380

Tyr Ser Ala Lys Gly Thr Gly Ser Ser Tyr Ser Trp Gly Thr Thr Asn
 385 390 395 400

Met Tyr His Pro Asp Ala Ile Asp Glu Gln Gly Asp Gly Lys Ile Arg
 405 410 415

Thr Gly Gly Pro Arg Tyr Arg Ser Ser Val Asn Thr Gln Gln Ser Val
 420 425 430

Thr Leu Gly Asp Thr Val Thr Phe Thr Pro Gln Trp Ser Ala Met Phe

435		440		445
Tyr Leu Ser Gln Ser Trp Leu Gln Thr Lys Asn Tyr Asp Lys His Gly				
450		455		460
Asn Gln Thr Asn Gln Val Asp Glu Asn Gly Leu Ser Pro Asn Ala Ala				
465		470		475
				480
Leu Met Tyr Lys Ile Thr Pro Asn Thr Met Ala Tyr Val Ser Tyr Ala				
		485		490
				495
Asp Ser Leu Glu Gln Gly Gly Thr Ala Pro Thr Asp Glu Ser Val Lys				
		500		510
Asn Ala Gly Gln Thr Leu Asn Pro Tyr Arg Ser Lys Gln Tyr Glu Val				
		515		525
Gly Leu Lys Ser Asp Ile Gly Glu Met Asn Leu Gly Ala Ala Leu Phe				
		530		540
Arg Leu Glu Arg Pro Phe Ala Tyr Leu Asp Thr Asp Asn Val Tyr Lys				
		545		555
				560
Glu Gln Gly Asn Gln Val Asn Asn Gly Leu Glu Leu Thr Ala Ala Gly				
		565		575
Asn Val Trp Gln Gly Leu Asn Ile Tyr Ser Gly Val Thr Phe Leu Asp				
		580		590
Pro Lys Leu Lys Asp Thr Ala Asn Ala Ser Thr Ser Asn Lys Gln Val				
		595		605
Val Gly Val Pro Lys Val Gln Ala Asn Leu Leu Ala Glu Tyr Ser Leu				
		610		620
Pro Ser Ile Pro Glu Trp Val Tyr Ser Ala Asn Val His Tyr Thr Gly				
		625		635
				640
Lys Arg Ala Ala Asn Asp Thr Asn Thr Ser Tyr Ala Ser Ser Tyr Thr				
		645		655
Thr Trp Asp Leu Gly Thr Arg Tyr Thr Thr Lys Val Ser Asn Val Pro				
		660		670

124

Thr Thr Phe Arg Val Val Val Asn Asn Val Phe Asp Lys His Tyr Trp
 675 680 685

Ala Ser Ile Phe Pro Ser Gly Thr Asp Gly Asp Asn Gly Ser Pro Ser
 690 695 700

Ala Phe Ile Gly Gly Gly Arg Glu Val Arg Ala Ser Val Thr Phe Asp
 705 710 715 720

Phe

<210> 50
 <211> 669
 <212> PRT
 <213> Escherichia coli
 <400> 50

Met Lys Asn Ile Thr Leu Trp Gln Arg Leu Arg Gln Val Ser Ile Ser
 1 5 10 15

Thr Ser Leu Arg Cys Ala Phe Leu Met Gly Ala Leu Leu Thr Leu Ile
 20 25 30

Val Ser Ser Val Ser Leu Tyr Ser Trp His Glu Gln Ser Ser Gln Ile
 35 40 45

Arg Tyr Ser Leu Asp Lys Tyr Phe Pro Arg Ile His Ser Ala Phe Leu
 50 55 60

Ile Glu Gly Asn Leu Asn Leu Val Val Asp Gln Leu Asn Glu Phe Leu
 65 70 75 80

Gln Ala Pro Asn Thr Thr Val Arg Leu Gln Leu Arg Thr Gln Ile Ile
 85 90 95

Gln His Leu Asp Thr Ile Glu Arg Leu Ser Arg Gly Leu Ser Ser Arg
 100 105 110

Glu Arg Gln Gln Leu Thr Val Ile Leu Gln Asp Ser Arg Ser Leu Leu
 115 120 125

Ser Glu Leu Asp Arg Ala Leu Tyr Asn Met Phe Leu Leu Arg Glu Lys

125

130

135

140

Val Ser Glu Leu Ser Ala Arg Ile Asp Trp Leu His Asp Asp Phe Thr
 145 150 155 160

Thr Glu Leu Asn Ser Leu Val Gln Asp Phe Thr Trp Gln Gln Gly Thr
 165 170 175

Leu Leu Asp Gln Ile Ala Ser Arg Gln Gly Asp Thr Ala Gln Tyr Leu
 180 185 190

Lys Arg Ser Arg Glu Val Gln Asn Glu Gln Gln Gln Val Tyr Thr Leu
 195 200 205

Ala Arg Ile Glu Asn Gln Ile Val Asp Asp Leu Arg Asp Arg Leu Asn
 210 215 220

Glu Leu Lys Ser Gly Arg Asp Asp Asp Ile Gln Val Glu Thr His Leu
 225 230 235 240

Arg Tyr Phe Glu Asn Leu Lys Lys Thr Ala Asp Glu Asn Ile Arg Met
 245 250 255

Leu Asp Asp Trp Pro Gly Thr Ile Thr Leu Arg Gln Thr Ile Asp Glu
 260 265 270

Leu Leu Asp Met Gly Ile Val Lys Asn Lys Met Pro Asp Thr Met Arg
 275 280 285

Glu Tyr Val Ala Ala Gln Lys Ala Leu Glu Asp Ala Ser Arg Thr Arg
 290 295 300

Glu Ala Thr Gln Gly Arg Phe Arg Thr Leu Leu Glu Ala Gln Leu Gly
 305 310 315 320

Ser Thr His Gln Gln Met Gln Met Phe Asn Gln Arg Met Glu Gln Ile
 325 330 335

Val His Val Ser Gly Gly Leu Ile Leu Val Ala Thr Ala Leu Ala Leu
 340 345 350

Leu Leu Ala Trp Val Phe Asn His Tyr Phe Ile Arg Ser Arg Leu Val
 355 360 365

126

Lys Arg Phe Thr Leu Leu Asn Gln Ala Val Val Gln Ile Gly Leu Gly
370 375 380

Gly Thr Glu Thr Thr Ile Pro Val Tyr Gly Asn Asp Glu Leu Gly Arg
385 390 395 400

Ile Ala Gly Leu Leu Arg His Thr Leu Gly Gln Leu Asn Val Gln Lys
405 410 415

Gln Gln Leu Glu Gln Glu Ile Thr Asp Arg Lys Val Ile Glu Ala Asp
420 425 430

Leu Arg Ala Thr Gln Asp Glu Leu Ile Gln Thr Ala Lys Leu Ala Val
435 440 445

Val Gly Gln Thr Met Thr Thr Leu Ala His Glu Ile Asn Gln Pro Leu
450 455 460

Asn Ala Leu Ser Met Tyr Leu Phe Thr Ala Arg Arg Ala Ile Glu Gln
465 470 475 480

Thr Gln Lys Glu Gln Ala Ser Met Met Leu Gly Lys Ala Glu Gly Val
485 490 495

Ile Ser Arg Ile Asp Ala Ile Ile Arg Ser Leu Arg Gln Phe Thr Arg
500 505 510

Arg Ala Glu Leu Glu Thr Ser Leu His Ala Val Asp Leu Ala Gln Met
515 520 525

Phe Ser Ala Ala Trp Glu Leu Leu Ala Met Arg His Arg Ser Leu Gln
530 535 540

Ala Thr Leu Val Leu Pro Gln Gly Thr Ala Thr Val Ser Gly Asp Glu
545 550 555 560

Val Arg Thr Gln Gln Val Leu Val Asn Val Leu Ala Asn Ala Leu Asp
565 570 575

Val Cys Gly Gln Gly Ala Val Ile Thr Val Asn Trp Gln Met Gln Gly
580 585 590

127

Lys Thr Leu Asn Val Phe Ile Gly Asp Asn Gly Pro Gly Trp Pro Glu
 595 600 605

Ala Leu Leu Pro Ser Leu Leu Lys Pro Phe Thr Thr Ser Lys Glu Val
 610 615 620

Gly Leu Gly Ile Gly Leu Ser Ile Cys Val Ser Leu Met Glu Gln Met
 625 630 635 640

Lys Gly Glu Leu Arg Leu Ala Ser Thr Met Thr Arg Asn Ala Cys Val
 645 650 655

Val Leu Gln Phe Arg Leu Thr Asp Val Glu Asp Ala Lys
 660 665

<210> 51
 <211> 753
 <212> PRT
 <213> Escherichia coli
 <400> 51

Met Asn Val Ile Lys Leu Ala Ile Gly Ser Gly Ile Leu Leu Leu Ser
 1 5 10 15

Cys Gly Ala Tyr Ser Gln Ser Ile Ser Glu Lys Thr Asn Ser Asp Lys
 20 25 30

Lys Gly Ala Ala Glu Phe Ser Pro Leu Ser Val Ser Val Gly Lys Thr
 35 40 45

Thr Ser Glu Gln Glu Ala Leu Glu Lys Thr Gly Ala Thr Ser Ser Arg
 50 55 60

Thr Thr Asp Lys Asn Leu Gln Ser Leu Asp Ala Thr Val Arg Ser Met
 65 70 75 80

Pro Gly Thr Tyr Thr Gln Ile Asp Pro Gly Gln Gly Ala Ile Ser Val
 85 90 95

Asn Ile Arg Gly Met Ser Gly Phe Gly Arg Val Asn Thr Met Val Asp
 100 105 110

Gly Ile Thr Gln Ser Phe Tyr Gly Thr Ser Thr Ser Gly Thr Thr Thr
 115 120 125

His Gly Ser Thr Asn Asn Met Ala Gly Val Leu Ile Asp Pro Asn Leu
 130 135 140

Leu Val Ala Val Asp Val Thr Arg Gly Asp Ser Ser Gly Ser Glu Gly
 145 150 155 160

Ile Asn Ala Leu Ala Gly Ser Ala Asn Met Arg Thr Ile Gly Val Asp
 165 170 175

Asp Val Ile Phe Asn Gly Asn Thr Tyr Gly Leu Arg Ser Arg Phe Ser
 180 185 190

Val Gly Ser Asn Gly Leu Gly Arg Ser Gly Met Ile Ala Leu Gly Gly
 195 200 205

Lys Ser Asp Ala Phe Thr Asp Thr Gly Ser Ile Gly Val Met Ala Ala
 210 215 220

Val Ser Gly Ser Ser Val Tyr Ser Asn Phe Ser Asn Gly Ser Gly Ile
 225 230 235 240

Asn Ser Lys Glu Phe Gly Tyr Asp Lys Tyr Met Lys Gln Asn Pro Lys
 245 250 255

Ser Gln Leu Tyr Lys Met Asp Ile Arg Pro Asp Glu Phe Asn Ser Phe
 260 265 270

Glu Leu Ser Ala Arg Thr Tyr Glu Asn Lys Phe Thr Arg Arg Asp Ile
 275 280 285

Thr Ser Asp Asp Tyr Tyr Ile Lys Tyr His Tyr Thr Pro Phe Ser Glu
 290 295 300

Leu Ile Asp Phe Asn Val Thr Ala Ser Thr Ser Arg Gly Asn Gln Lys
 305 310 315 320

Tyr Arg Asp Gly Ser Leu Tyr Thr Phe Tyr Lys Thr Ser Ala Gln Asn
 325 330 335

Arg Ser Asp Ala Leu Asp Ile Asn Asn Thr Ser Arg Phe Thr Val Ala
 340 345 350

Asp Asn Asp Leu Glu Phe Met Leu Gly Ser Lys Leu Met Arg Thr Arg
 355 360 365

Tyr Asp Arg Thr Ile His Ser Ala Ala Gly Asp Pro Lys Ala Asn Gln
 370 375 380

Glu Ser Ile Glu Asn Asn Pro Phe Ala Pro Ser Gly Gln Gln Asp Ile
 385 390 395 400

Ser Ala Leu Tyr Thr Gly Leu Lys Val Thr Arg Gly Ile Trp Glu Ala
 405 410 415

Asp Phe Asn Leu Asn Tyr Thr Arg Asn Arg Ile Thr Gly Tyr Lys Pro
 420 425 430

Ala Cys Asp Ser Arg Val Ile Cys Val Pro Gln Gly Ser Tyr Asp Ile
 435 440 445

Asp Asp Lys Glu Gly Gly Phe Asn Pro Ser Val Gln Leu Ser Ala Gln
 450 455 460

Val Thr Pro Trp Leu Gln Pro Phe Ile Gly Tyr Ser Lys Ser Met Arg
 465 470 475 480

Ala Pro Asn Ile Gln Glu Met Phe Phe Ser Asn Ser Gly Gly Ala Ser
 485 490 495

Met Asn Pro Phe Leu Lys Pro Glu Arg Ala Glu Thr Trp Gln Ala Gly
 500 505 510

Phe Asn Ile Asp Thr Arg Asp Leu Leu Val Glu Gln Asp Ala Leu Arg
 515 520 525

Phe Lys Ala Leu Ala Tyr Arg Ser Arg Ile Gln Asn Tyr Ile Tyr Ser
 530 535 540

Glu Ser Tyr Leu Val Cys Ser Gly Gly Arg Lys Cys Ser Leu Pro Glu
 545 550 555 560

Val Ile Gly Asn Gly Trp Glu Gly Ile Ser Asp Glu Tyr Ser Asp Asn
 565 570 575

130

Met Tyr Ile Tyr Val Asn Ser Ala Ser Asp Val Ile Ala Lys Gly Phe
 580 585 590

Glu Leu Glu Met Asp Tyr Asp Ala Gly Phe Ala Phe Gly Arg Leu Ser
 595 600 605

Phe Ser Gln Gln Gln Thr Asp Gln Pro Thr Ser Ile Ala Ser Thr His
 610 615 620

Phe Gly Ala Gly Asp Ile Thr Glu Leu Pro Arg Lys Tyr Met Thr Leu
 625 630 635 640

Asp Thr Gly Val Arg Phe Phe Asp Asn Ala Leu Thr Leu Gly Thr Ile
 645 650 655

Ile Lys Tyr Thr Gly Lys Ala Arg Arg Leu Ser Pro Asp Phe Glu Gln
 660 665 670

Asp Glu His Thr Gly Ala Ile Ile Lys Gln Asp Leu Pro Gln Ile Pro
 675 680 685

Thr Ile Ile Asp Leu Tyr Gly Thr Tyr Glu Tyr Asn Arg Asn Leu Thr
 690 695 700

Leu Lys Leu Ser Val Gln Asn Leu Met Asn Arg Asp Tyr Ser Glu Ala
 705 710 715 720

Leu Asn Lys Leu Asn Met Met Pro Gly Leu Gly Asp Glu Thr His Pro
 725 730 735

Ala Asn Ser Ala Arg Gly Arg Thr Trp Ile Phe Gly Gly Asp Ile Arg
 740 745 750

Phe

<210> 52
 <211> 133
 <212> PRT
 <213> Escherichia coli
 <400> 52

Met Ser Ser Lys Thr Lys Cys Trp Leu Trp Met Leu Leu Val Ile Leu
 1 5 10 15

131

Ser Glu Thr Ser Ala Thr Ser Thr Leu Lys Met Phe Asp Asn Ser Glu
20 25 30

Gly Met Thr Lys Thr Leu Leu Leu Ala Leu Ile Val Val Leu Tyr Cys
35 40 45

Ile Cys Tyr Tyr Ser Leu Ser Arg Ala Val Lys Asp Ile Pro Val Gly
50 55 60

Leu Ala Tyr Ala Thr Trp Ser Gly Thr Gly Ile Leu Met Val Ser Thr
65 70 75 80

Leu Gly Ile Leu Phe Tyr Gly Gln His Pro Asp Thr Ala Ala Ile Ile
85 90 95

Gly Met Val Ile Ile Ala Ser Gly Ile Ile Ile Met Asn Leu Phe Ser
100 105 110

Lys Met Gly Ser Glu Glu Ala Glu Glu Thr Pro Val Thr Asn Leu Asp
115 120 125

Lys Lys Ile Ala Asn
130

<210> 53
<211> 286
<212> PRT
<213> Escherichia coli
<400> 53

Met Tyr Ile Lys Lys His Trp Ile Ala Leu Ser Ile Leu Leu Ile Pro
1 5 10 15

Cys Ile Gly Asn Ala Gln Glu Ile Lys Ile Asp Glu Ser Trp Leu His
20 25 30

Gln Ser Leu Asn Val Ile Gly Arg Thr Asp Ser Arg Phe Gly Pro Arg
35 40 45

Leu Thr Asn Asp Leu Tyr Pro Glu Tyr Thr Val Ala Gly Arg Lys Asp
50 55 60

Trp Phe Asp Phe Tyr Gly Tyr Val Asp Leu Pro Lys Phe Phe Gly Val
65 70 75 80

132

Gly Ser His Tyr Asp Val Gly Ile Trp Asp Glu Gly Ser Pro Leu Phe
85 90 95

Thr Glu Ile Glu Pro Arg Phe Ser Ile Asp Lys Leu Thr Gly Leu Asn
100 105 110

Leu Ala Phe Gly Pro Phe Lys Glu Trp Phe Ile Ala Asn Asn Tyr Val
115 120 125

Tyr Asp Met Gly Asp Asn Gln Ser Ser Arg Gln Ser Thr Trp Tyr Met
130 135 140

Gly Leu Gly Thr Asp Ile Asp Thr Gly Leu Pro Ile Lys Leu Ser Ala
145 150 155 160

Asn Ile Tyr Ala Lys Tyr Gln Trp Gln Asn Tyr Gly Ala Ala Asn Glu
165 170 175

Asn Glu Trp Asp Gly Tyr Arg Phe Lys Ile Lys Tyr Ser Ile Pro Leu
180 185 190

Thr Asn Leu Phe Gly Gly Arg Leu Val Tyr Asn Ser Phe Thr Asn Phe
195 200 205

Asp Phe Gly Ser Asp Leu Ala Asp Lys Ser His Asn Asn Lys Arg Thr
210 215 220

Ser Asn Ala Ile Ala Ser Ser His Ile Leu Ser Leu Leu Tyr Glu His
225 230 235 240

Trp Lys Phe Ala Phe Thr Leu Arg Tyr Phe His Asn Gly Gly Gln Trp
245 250 255

Asn Ala Gly Glu Lys Val Asn Phe Gly Asp Gly Pro Phe Glu Leu Lys
260 265 270

Asn Thr Gly Trp Gly Thr Tyr Thr Thr Ile Gly Tyr Gln Phe
275 280 285

<210> 54
<211> 172
<212> PRT

133

<213> Escherichia coli
<400> 54

Met Arg Ile Ala Pro Arg Thr Phe Phe Ala Ile Ser Ala Leu Ala Phe
1 5 10 15

Ile Val Ala Ser Gly Phe Ser Phe Trp Arg Leu Ser Pro Ala Glu Asn
20 25 30

Thr Gly Ile Met Ser Cys Ser Thr Lys Gly Ile Met Arg Phe Glu Asn
35 40 45

Met Glu Lys Glu Asn Val Asn Gly Asn Ile His Phe Asn Phe Gly Ser
50 55 60

Gln Gly Lys Gly Ser Met Val Leu Glu Gly Tyr Thr Asp Ser Ala Ala
65 70 75 80

Gly Trp Leu Tyr Leu Gln Arg Tyr Val Lys Phe Thr Tyr Thr Ser Lys
85 90 95

Arg Val Ser Ala Thr Glu Arg His Tyr Arg Ile Ser Gln Trp Glu Ser
100 105 110

Ser Ala Ser Ser Ile Asp Glu Ser Pro Asp Val Ile Phe Asp Tyr Phe
115 120 125

Met Arg Glu Met Ser Asp Ser His Asp Gly Leu Phe Leu Asn Ala Gln
130 135 140

Lys Leu Asn Asp Lys Ala Ile Leu Leu Ser Ser Ile Asn Ser Pro Leu
145 150 155 160

Trp Ile Cys Thr Leu Lys Ser Gly Ser Lys Leu Asp
165 170

<210> 55
<211> 182
<212> PRT
<213> Escherichia coli
<400> 55

Met Lys Ile Lys Val Ile Ala Leu Ala Thr Phe Val Ser Ala Val Phe
1 5 10 15

134

Ala Gly Ser Ala Met Ala Tyr Asp Gly Thr Ile Thr Phe Thr Gly Lys
 20 25 30

Val Val Ala Gln Thr Cys Thr Val Asn Thr Ser Asp Lys Asp Leu Ala
 35 40 45

Val Thr Leu Pro Thr Val Ala Thr Ser Ser Leu Lys Asp Asn Ala Ala
 50 55 60

Thr Ser Gly Leu Thr Pro Phe Ala Ile Arg Leu Thr Gly Cys Ala Thr
 65 70 75 80

Gly Met Asn Ser Ala Gln Asn Val Lys Ala Tyr Phe Glu Pro Ser Ser
 85 90 95

Asn Ile Asp Leu Ala Thr His Asn Leu Lys Asn Thr Ala Thr Pro Thr
 100 105 110

Lys Ala Asp Asn Val Gln Ile Gln Leu Leu Asn Ser Asn Gly Thr Ser
 115 120 125

Thr Ile Leu Leu Gly Glu Ala Asp Asn Gly Gln Asp Val Gln Ser Glu
 130 135 140

Thr Ile Gly Ser Asp Gly Ser Ala Thr Leu Arg Tyr Met Ala Gln Tyr
 145 150 155 160

Tyr Ala Thr Gly Gln Ser Thr Ala Gly Asp Val Lys Ala Thr Val His
 165 170 175

Tyr Thr Ile Ala Tyr Glu
 180

<210> 56

<211> 359

<212> PRT

<213> Escherichia coli

<400> 56

Met Lys Arg Ile Phe Phe Ile Pro Leu Phe Leu Ile Leu Leu Pro Lys
 1 5 10 15

Leu Ala Val Ala Gly Pro Asp Asp Tyr Val Pro Ser Gln Ile Ala Val
 20 25 30

135

Asn Thr Ser Thr Leu Pro Gly Val Val Ile Gly Pro Ala Asp Ala His
 35 40 45

Thr Tyr Pro Arg Val Ile Gly Glu Leu Ala Gly Thr Ser Asn Gln Tyr
 50 55 60

Val Phe Asn Gly Gly Ala Ile Ala Leu Met Arg Gly Lys Phe Thr Pro
 65 70 75 80

Ala Leu Pro Lys Ile Gly Ser Ile Thr Val Tyr Phe Pro Ser Arg Lys
 85 90 95

Gln Arg Asp Ser Ser Asp Phe Asp Ile Tyr Asp Ile Gly Val Ser Gly
 100 105 110

Leu Gly Ile Ile Ile Gly Met Ala Gly Tyr Trp Pro Ala Thr Pro Leu
 115 120 125

Val Pro Ile Asn Ser Ser Gly Ile Tyr Ile Asp Pro Val Gly Ala Asn
 130 135 140

Thr Asn Pro Asn Thr Tyr Asn Gly Ala Thr Ala Ser Phe Gly Ala Arg
 145 150 155 160

Leu Phe Val Ala Phe Val Ala Thr Gly Arg Leu Pro Asn Gly Tyr Ile
 165 170 175

Thr Ile Pro Thr Arg Gln Leu Gly Thr Ile Leu Leu Glu Ala Lys Arg
 180 185 190

Thr Ser Leu Asn Asn Lys Gly Leu Thr Ala Pro Val Met Leu Asn Gly
 195 200 205

Gly Arg Ile Gln Val Gln Ser Gln Thr Cys Thr Met Gly Gln Lys Asn
 210 215 220

Tyr Val Val Pro Leu Asn Thr Val Tyr Gln Ser Gln Phe Thr Ser Leu
 225 230 235 240

Tyr Lys Glu Ile Gln Gly Gly Lys Ile Asp Ile His Leu Gln Cys Pro
 245 250 255

136

Asp Gly Ile Asp Val Tyr Ala Thr Leu Thr Asp Ala Ser Gln Pro Val
 260 265 270

Asn Arg Thr Asp Ile Leu Thr Leu Ser Ser Glu Ser Thr Ala Lys Gly
 275 280 285

Phe Gly Ile Arg Leu Tyr Lys Asp Ser Asp Val Thr Ala Ile Ser Tyr
 290 295 300

Gly Glu Asp Ser Pro Val Lys Gly Asn Gly Ser Gln Trp His Phe Ser
 305 310 315 320

Asp Tyr Arg Gly Glu Val Asn Pro His Ile Asn Leu Arg Ala Asn Tyr
 325 330 335

Ile Lys Ile Ala Asp Ala Thr Thr Pro Gly Ser Val Lys Ala Ile Ala
 340 345 350

Thr Ile Thr Phe Ser Tyr Gln
 355

<210> 57

<211> 844

<212> PRT

<213> Escherichia coli

<400> 57

Met Asn Ala Asn Asn Leu Ser Cys Leu Ile Tyr Cys Arg Cys Ser Leu
 1 5 10 15

Leu Leu Phe Ala Ala Leu Gly Leu Thr Val Thr Asn His Ser Phe Ala
 20 25 30

Ala Glu Glu Ala Glu Phe Asp Ser Glu Phe Leu His Leu Asp Lys Gly
 35 40 45

Ile Asn Ala Ile Asp Ile Arg Arg Phe Ser His Gly Asn Pro Val Pro
 50 55 60

Glu Gly Arg Tyr Tyr Ser Asp Ile Tyr Val Asn Asn Val Trp Lys Gly
 65 70 75 80

Lys Ala Asp Leu Gln Tyr Leu Arg Thr Ala Asn Thr Gly Ala Pro Thr
 85 90 95

137

Leu Cys Leu Thr Pro Glu Leu Leu Ser Leu Ile Asp Leu Val Lys Asp
 100 105 110

Thr Met Ser Gly Asn Thr Ser Cys Phe Pro Ala Ser Thr Gly Leu Ser
 115 120 125

Ser Ala Arg Ile Asn Phe Asp Leu Ser Thr Leu Arg Leu Asn Ile Glu
 130 135 140

Ile Pro Gln Ala Leu Leu Asn Thr Arg Pro Arg Gly Tyr Ile Ser Pro
 145 150 155 160

Ala Gln Trp Gln Ser Gly Val Pro Ala Ala Phe Ile Asn Tyr Asp Ala
 165 170 175

Asn Tyr Tyr Gln Tyr Ser Ser Ser Gly Thr Ser Asn Glu Gln Thr Tyr
 180 185 190

Leu Gly Leu Lys Ala Gly Phe Asn Leu Trp Gly Trp Ala Leu Arg His
 195 200 205

Arg Gly Ser Glu Ser Trp Asn Asn Ser Tyr Pro Ala Gly Tyr Gln Asn
 210 215 220

Ile Glu Thr Ser Ile Met His Asp Leu Ala Pro Leu Arg Ala Gln Phe
 225 230 235 240

Thr Leu Gly Asp Phe Tyr Thr Asn Gly Glu Leu Met Asp Ser Leu Ser
 245 250 255

Leu Arg Gly Val Arg Leu Ala Ser Asp Glu Arg Met Leu Pro Gly Ser
 260 265 270

Leu Arg Gly Tyr Ala Pro Ala Val Arg Gly Ile Ala Asn Ser Asn Ala
 275 280 285

Lys Val Thr Ile Tyr Gln Asn Ala His Ile Leu Tyr Glu Thr Thr Val
 290 295 300

Pro Ala Gly Pro Phe Val Ile Asn Asp Leu Tyr Pro Ser Gly Tyr Ala
 305 310 315 320

138

Gly Asp Leu Leu Val Lys Ile Thr Glu Ser Asn Gly Gln Thr Arg Met
 325 330 335

Phe Thr Val Pro Phe Ala Ala Val Ala Gln Leu Ile Arg Pro Gly Phe
 340 345 350

Ser Arg Trp Gln Met Ser Val Gly Lys Tyr Arg Tyr Ala Asn Lys Thr
 355 360 365

Tyr Asn Asp Leu Ile Ala Gln Gly Thr Tyr Gln Tyr Gly Leu Thr Asn
 370 375 380

Asp Ile Thr Leu Asn Ser Gly Leu Thr Thr Ala Ser Gly Tyr Thr Ala
 385 390 395 400

Gly Leu Ala Gly Leu Ala Phe Asn Thr Pro Leu Gly Ala Ile Ala Ser
 405 410 415

Asp Ile Thr Leu Ser Arg Thr Ala Phe Arg Tyr Ser Gly Val Thr Arg
 420 425 430

Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser
 435 440 445

Asn Thr Asn Ile Thr Leu Ala Ala Tyr Arg Tyr Ser Ser Lys Asp Phe
 450 455 460

Tyr His Leu Lys Asp Ala Leu Ser Ala Asn His Asn Ala Phe Ile Asp
 465 470 475 480

Asp Val Ser Val Lys Ser Thr Ala Phe Tyr Arg Pro Arg Asn Gln Phe
 485 490 495

Gln Ile Ser Ile Asn Gln Glu Leu Gly Glu Lys Trp Gly Gly Met Tyr
 500 505 510

Leu Thr Gly Thr Thr Tyr Asn Tyr Trp Gly His Lys Gly Ser Arg Asn
 515 520 525

Glu Tyr Gln Ile Gly Tyr Ser Asn Phe Trp Lys Gln Leu Gly Tyr Gln
 530 535 540

Ile Gly Leu Ser Gln Ser Arg Asp Asn Glu Gln Gln Arg Arg Asp Asp

139

545	550	555	560
Arg Phe Tyr Ile Asn Phe Thr Leu Pro Leu Gly Gly Ser Val Gln Ser	565	570	575
Pro Val Phe Ser Thr Val Leu Asn Tyr Ser Lys Glu Glu Lys Asn Ser	580	585	590
Ile Gln Thr Ser Ile Ser Gly Thr Gly Gly Glu Asp Asn Gln Phe Ser	595	600	605
Tyr Gly Ile Ser Gly Asn Ser Gln Glu Asn Gly Pro Ser Gly Tyr Ala	610	615	620
Met Asn Gly Gly Tyr Arg Ser Pro Tyr Val Asn Ile Thr Thr Thr Val	625	630	635
Gly His Asp Thr Gln Asn Asn Asn Gln Arg Ser Phe Gly Ala Ser Gly	645	650	655
Ala Val Val Ala His Pro Tyr Gly Val Thr Leu Ser Asn Asp Leu Ser	660	665	670
Asp Thr Phe Ala Ile Ile His Ala Glu Gly Ala Gln Gly Ala Val Ile	675	680	685
Asn Asn Ala Ser Gly Ser Arg Leu Asp Phe Trp Gly Asn Gly Val Val	690	695	700
Pro Tyr Val Thr Pro Tyr Glu Lys Asn Gln Ile Ser Ile Asp Pro Ser	705	710	715
Asn Leu Asp Leu Asn Val Glu Leu Ser Ala Thr Glu Gln Glu Ile Ile	725	730	735
Pro Arg Ala Asn Ser Ala Thr Leu Val Lys Phe Asp Thr Lys Thr Gly	740	745	750
Arg Ser Leu Leu Phe Asp Ile Arg Met Ser Thr Gly Asn Pro Pro Pro	755	760	765
Met Ala Ser Glu Val Leu Asp Glu His Gly Gln Leu Ala Gly Tyr Val	770	775	780

140

Ala Gln Ala Gly Lys Val Phe Thr Arg Gly Leu Pro Glu Lys Gly His
785 790 795 800

Leu Ser Val Val Trp Gly Pro Asp Asn Lys Asp Arg Cys Ser Phe Val
805 810 815

Tyr His Val Ala His Asn Lys Asp Asp Met Gln Ser Gln Leu Val Pro
820 825 830

Val Leu Cys Ile Gln His Pro Asn Gln Glu Lys Thr
835 840

<210> 58
<211> 277
<212> PRT
<213> Escherichia coli
<400> 58

Met Val Lys Cys His Thr Leu Ile Asn Arg Arg Asn Lys Cys Leu Leu
1 5 10 15

Ile Val Phe Ile Val Leu Ile Gly Trp Ile Ile Phe Arg Pro Lys Ala
20 25 30

Tyr Thr Tyr Ser Leu Asn Asp Lys Glu Lys Glu Met Leu Ile Met Leu
35 40 45

Ser Gln His Pro Glu Thr Arg Tyr Phe Gly Phe Tyr Ser Ile Glu Leu
50 55 60

Pro Ala Asp Tyr Lys Pro Thr Gly Met Val Met Phe Ile Gln Gly Ser
65 70 75 80

Ala Met Ile Pro Val Glu Thr Lys Leu Gln Tyr Tyr Pro Pro Phe Leu
85 90 95

Gln Tyr Met Thr Arg Tyr Glu Ala Glu Leu Lys Asn Thr Ser Ala Leu
100 105 110

Asp Pro Leu Asp Thr Pro Tyr Leu Lys Gln Val His Pro Leu Ser Pro
115 120 125

Pro Met Asn Gly Val Ile Phe Glu Arg Met Lys Ala Lys Tyr Thr Pro

141

130

135

140

Asp Phe Ala Arg Val Leu Asp Ala Trp Lys Trp Glu Asn Gly Val Thr
 145 150 155 160

Phe Ser Val Lys Ile Glu Ala Lys Asp Gly Arg Ala Thr Arg Tyr Asp
 165 170 175

Gly Ile Ser Lys Ile Ala Glu Tyr Ser Tyr Gly Tyr Asn Ile Pro Glu
 180 185 190

Lys Lys Val Gln Leu Leu Thr Ile Leu Ser Gly Leu Gln Pro Arg Ala
 195 200 205

Asp Asn Gln Pro Pro Ser Glu Asn Lys Leu Ala Ile Gln Tyr Ala Gln
 210 215 220

Val Asp Ala Ser Leu Leu Gly Glu Tyr Glu Leu Ser Val Asp Tyr Lys
 225 230 235 240

Asn Ser Asn Asn Ile Lys Ile Ser Leu Gln Thr Asp Asn Asn Ser Tyr
 245 250 255

Ile Asp Ser Leu Leu Asp Ile Arg Tyr Pro Ser Asn Gly Asn Arg Ala
 260 265 270

Trp Tyr Asn Ser Ile
 275

<210> 59

<211> 366

<212> PRT

<213> Escherichia coli

<400> 59

Met Leu Pro Glu Pro Val Tyr Arg Arg Trp Ile Ile Leu Leu Ile Ser
 1 5 10 15

Met Leu Thr Val Gly Thr Leu Phe Ile Leu Ser Val Trp Asn Ser Ala
 20 25 30

Thr Tyr Trp Asp Ile Phe Ile Tyr Gly Val Leu Pro Met Leu Phe Leu
 35 40 45

142

Trp Leu Cys Leu Phe Gly Ile Ala Leu Asn Lys Tyr Glu Gln Ser Val
 50 55 60

Ala Ala Cys Ile Ser Trp Glu Ser Glu Arg Gln Gln Val Lys Gln Leu
 65 70 75 80

Trp Gln His Trp Ser Gln Lys Gln Leu Ala Ile Val Gly Asn Val Leu
 85 90 95

Phe Thr Pro Glu Glu Lys Gly Met Ser Val Leu Leu Gly Pro Gln Glu
 100 105 110

Glu Ile Pro Ala Tyr Pro Lys Lys Ala Arg Pro Leu Phe Ser Ala Ser
 115 120 125

Arg Tyr Ser Leu Ser Ser Ile Phe His Asp Ile His Gln Gln Leu Thr
 130 135 140

Gln Gln Phe Pro Asp Tyr Arg His Tyr Leu His Thr Ile Tyr Val Leu
 145 150 155 160

Gln Pro Glu Lys Trp Arg Gly Glu Thr Val Arg Gln Ala Ile Phe His
 165 170 175

Gln Trp Asp Leu Val Pro Glu Arg Thr Asn Thr Leu Asn Gln Ile Gln
 180 185 190

Ser Leu Tyr Asp Glu Arg Phe Asp Gly Leu Ile Leu Val Val Cys Leu
 195 200 205

Gln Asn Trp Pro Glu Asn Lys Pro Glu Asp Thr Ser Glu Leu Val Ser
 210 215 220

Ala Gln Leu Ile Ser Ser Ser Ser Phe Val Arg Gln His Gln Ile Pro
 225 230 235 240

Val Ile Ala Gly Leu Gly Arg Val Met Pro Leu Glu Pro Glu Glu Leu
 245 250 255

Glu His Asn Leu Asp Val Leu Phe Glu Tyr Asn Gln Leu Asp Asn Lys
 260 265 270

Gln Leu Gln His Val Trp Val Ser Gly Leu Asp Glu Gly Thr Ile Glu

143

275

280

285

Asn Leu Met Gln Tyr Ala Glu Gln His Gln Trp Ser Leu Pro Lys Lys
 290 295 300

Arg Pro Leu His Met Ile Asp His Ser Phe Gly Pro Thr Gly Glu Phe
 305 310 315 320

Ile Phe Pro Val Ser Leu Ala Met Leu Ser Glu Ala Ala Lys Glu Thr
 325 330 335

Glu Gln Asn His Leu Ile Ile Tyr Gln Ser Ala Gln Tyr Ala Gln Lys
 340 345 350

Lys Ser Leu Cys Leu Ile Thr Arg Lys Leu Tyr Leu Arg Thr
 355 360 365

<210> 60

<211> 260

<212> PRT

<213> Escherichia coli

<400> 60

Met Leu Asn Arg Lys Leu Asn Ile Arg Leu Arg His Ser Leu Asn Ser
 1 5 10 15

His Cys Ile Pro Ser Ile Ile Ile Asn Asn Thr Val Arg Ser Phe Gln
 20 25 30

Arg Ser Val Met Asn Thr Arg Ala Leu Phe Pro Leu Leu Phe Thr Val
 35 40 45

Ala Ser Phe Ser Ala Ser Ala Gly Asn Trp Ala Val Lys Asn Gly Trp
 50 55 60

Cys Gln Thr Met Thr Glu Asp Gly Gln Ala Leu Val Met Leu Lys Asn
 65 70 75 80

Gly Thr Ile Gly Ile Thr Gly Leu Met Gln Gly Cys Pro Asn Gly Val
 85 90 95

Gln Thr Leu Leu Gly Ser Arg Ile Ser Ile Asn Gly Asn Leu Ile Pro
 100 105 110

144

Thr Ser Gln Met Cys Asn Gln Gln Thr Gly Phe Arg Ala Val Glu Val
 115 120 125

Glu Ile Gly Gln Ala Pro Glu Met Val Lys Lys Ala Val His Ser Ile
 130 135 140

Ala Glu Arg Asp Val Ser Val Leu Gln Ala Phe Gly Val Arg Met Glu
 145 150 155 160

Phe Thr Arg Gly Asp Met Leu Lys Val Cys Pro Lys Phe Val Thr Ser
 165 170 175

Leu Ala Gly Phe Ser Pro Lys Gln Thr Thr Thr Ile Asn Lys Asp Ser
 180 185 190

Val Leu Gln Ala Ala Arg Gln Ala Tyr Ala Arg Glu Tyr Asp Glu Glu
 195 200 205

Thr Thr Glu Thr Ala Asp Phe Gly Ser Tyr Glu Val Lys Gly Asn Lys
 210 215 220

Val Glu Phe Glu Val Phe Asn Pro Glu Asp Arg Ala Tyr Asp Lys Val
 225 230 235 240

Thr Val Thr Val Gly Ala Asp Gly Asn Ala Thr Gly Ala Ser Val Glu
 245 250 255

Phe Ile Gly Lys
 260

<210> 61
 <211> 385
 <212> PRT
 <213> Escherichia coli
 <400> 61

Val Val Ile Ile Asn Ser Thr Ile Leu Ser Gly Ala Gly Ala Ile Pro
 1 5 10 15

Ser Leu Thr Ser Leu Leu Pro Asp Ile Arg Lys Met Leu Leu Val Thr
 20 25 30

Asp Arg Asn Ile Ala Gln Leu Asp Gly Val Gln Gln Ile Arg Ala Leu
 35 40 45

145

Leu Glu Lys His Cys Pro Gln Val Asn Val Ile Asp Asn Val Pro Ala
 50 55 60

Glu Pro Thr His His Asp Val Arg Gln Leu Met Asp Ala Pro Gly Asp
 65 70 75 80

Ala Ser Phe Asp Val Val Val Gly Ile Gly Gly Gly Ser Val Leu Asp
 85 90 95

Val Ala Lys Leu Leu Ser Val Leu Cys His Pro Gln Ser Pro Gly Leu
 100 105 110

Asp Ala Leu Leu Ala Gly Glu Lys Pro Thr Gln Arg Val Gln Ser Trp
 115 120 125

Leu Ile Pro Thr Thr Ala Gly Thr Gly Ser Glu Ala Thr Pro Asn Ala
 130 135 140

Ile Leu Ala Ile Pro Glu Gln Ser Thr Lys Val Gly Ile Ile Ser Gln
 145 150 155 160

Val Leu Leu Pro Asp Tyr Val Ala Leu Phe Pro Glu Leu Thr Thr Ser
 165 170 175

Met Pro Ala His Ile Ala Ala Ser Thr Gly Ile Asp Ala Leu Cys His
 180 185 190

Leu Leu Glu Cys Phe Thr Ala Thr Val Ala Asn Pro Val Ser Asp Asn
 195 200 205

Ala Ala Leu Thr Gly Leu Ser Lys Leu Phe Arg His Ile Gln Pro Ala
 210 215 220

Val Asn Asp Pro Gln Asp Leu Arg Ala Lys Leu Glu Met Leu Trp Ala
 225 230 235 240

Ser Tyr Tyr Gly Gly Val Ala Ile Thr His Ala Gly Thr His Leu Val
 245 250 255

His Ala Leu Ser Tyr Pro Leu Gly Gly Lys Tyr His Leu Pro His Gly
 260 265 270

146

Val Ala Asn Ala Ile Leu Leu Ala Pro Cys Met Ala Phe Val Arg Pro
 275 280 285

Trp Ala Val Glu Lys Phe Ala Arg Val Trp Asp Cys Ile Pro Asp Ala
 290 295 300

Glu Thr Ala Leu Ser Ala Glu Glu Lys Ser His Ala Leu Val Thr Trp
 305 310 315 320

Leu Gln Ala Leu Val Asn Gln Leu Lys Leu Pro Asn Asn Leu Ala Ala
 325 330 335

Leu Gly Val Pro Pro Glu Asp Ile Ala Ser Leu Ser Glu Ala Ala Leu
 340 345 350

Asn Val Lys Arg Leu Met Asn Asn Val Pro Cys Gln Ile Asp Leu Gln
 355 360 365

Asp Val Gln Ala Ile Tyr Gln Thr Leu Phe Pro Gln His Pro Phe Lys
 370 375 380

Glu
 385

<210> 62
 <211> 105
 <212> PRT
 <213> Escherichia coli
 <400> 62

Met Asn Ile Arg Lys Leu Phe Cys Pro Gly Asn Thr Pro Arg Ile Leu
 1 5 10 15

Leu Phe Leu Phe Phe Phe Val Val Ser Ala Ile Thr Thr Ile Ala Cys
 20 25 30

Gly Tyr Thr Glu Lys Asn Ala Thr Gly Asn Val Leu Leu Leu Phe Leu
 35 40 45

Leu Leu Leu Leu Ala His Arg Asn Thr Leu Thr Ser Ile Thr Ala Leu
 50 55 60

Leu Phe Leu Phe Cys Cys Ala Leu Tyr Ala Pro Ala Gly Met Thr Tyr
 65 70 75 80

147

Gly Lys Ile Asn Asn Ser Phe Ile Val Ala Leu Leu Gln Thr Thr Thr
 85 90 95

Asp Glu Ala Ala Glu Phe Thr Gly Met
 100 105

<210> 63
 <211> 147
 <212> PRT
 <213> Escherichia coli
 <400> 63

Met Asn Ile Gln Ala Ile Lys Glu Met Val Asn Leu Ile Cys Ser Phe
 1 5 10 15

Leu Phe Ile Phe Phe Leu Ser Ser Ala Phe Val Ser Phe Gly Cys Tyr
 20 25 30

Ala Ile Tyr Glu Leu Phe Leu Trp Asn Asp Ile Ile Val Tyr Ser Trp
 35 40 45

Gly Tyr Ile Leu Ile Val Phe Leu Pro Phe Thr Leu Tyr Val Met Ser
 50 55 60

Phe Glu Ile Leu Phe Phe Ala Ile Ser Gly Arg Arg Leu Ser Lys Val
 65 70 75 80

Thr Met Val Arg Leu Trp Leu Ile Ile Lys Ile Ile Ile Ala Phe Ser
 85 90 95

Ile Cys Ala Val Leu Ile Phe Ser Ser Ile Tyr Lys Lys Glu Leu Leu
 100 105 110

Ser Arg Asn Tyr Ile Ala Cys Ser Gly Ile Pro Ser Gly Trp Met Pro
 115 120 125

Gly Leu Ala Thr Lys Tyr Val Lys Glu Lys Ser Leu Cys Glu Lys Asn
 130 135 140

Gly Asn Asn
 145

<210> 64
 <211> 178

148

<212> PRT

<213> Escherichia coli

<400> 64

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
 1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
 20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
 35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
 50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
 65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
 85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
 100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
 115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
 130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
 145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
 165 170 175

Asp Lys

<210> 65

<211> 209

<212> PRT

<213> Escherichia coli

<400> 65

149

Met Phe Leu Lys Arg Lys Trp Tyr Tyr Ala Val Thr Thr Ser Val Val
 1 5 10 15

Ile Thr Leu Cys Gly Gly Gly Tyr Tyr Met Tyr Arg Gln Glu Tyr Gln
 20 25 30

Met Val Val Thr Val Pro Thr Ala Asp Ala Asn Asp Pro Asn Trp Pro
 35 40 45

Asn Lys Arg Ile Gln Phe Asp Thr Ser Glu Trp Leu Gln Gln Leu Gln
 50 55 60

Tyr Ile Lys Ile Asp Asp His Tyr Ile Leu Asn Thr Gln Tyr Thr Pro
 65 70 75 80

Ile Ala Asn Leu Asp Asp Phe Gly Ile Thr Leu Lys Leu Gln Asn Ala
 85 90 95

Leu Asn Gly Ser Asp Lys Arg Leu Pro Ala Leu Tyr Gly Leu Ala Glu
 100 105 110

Met Asp Ala Gln Lys Phe Lys Asp Leu Met Arg Gly Lys Ile Lys Cys
 115 120 125

Glu Tyr Leu Arg Thr Thr Phe Asp Ala Glu Thr Leu Lys Pro Val Asn
 130 135 140

Asp Tyr Phe Leu Ile Ser Phe Thr Tyr Lys Asp Lys Trp Tyr Glu Phe
 145 150 155 160

Glu Thr Glu Arg Lys Ile Ser Lys Thr Ser Asp Asp Gly Tyr Phe Leu
 165 170 175

Trp Ala Phe Asp Asn Thr Val His Glu Ala Gly Tyr Trp His Asn Thr
 180 185 190

Asp Pro Ala Ala Tyr Ser Tyr Arg Asp Tyr Gln Asn Gly Lys Ala Val
 195 200 205

Lys

150

<210> 66
 <211> 424
 <212> PRT
 <213> Escherichia coli
 <400> 66

Met Asp Ile Trp Arg Gly His Ser Phe Leu Met Thr Ile Ser Ala Arg
 1 5 10 15

Phe Arg Gln Tyr Val Phe Ser Leu Met Ser Ile Leu Leu Gln Glu Arg
 20 25 30

Lys Met Asn Ile Phe Thr Leu Ser Lys Ala Pro Leu Tyr Leu Leu Ile
 35 40 45

Ser Leu Phe Leu Pro Thr Met Ala Met Ala Ile Asp Pro Pro Glu Arg
 50 55 60

Glu Leu Ser Arg Phe Ala Leu Lys Thr Asn Tyr Leu Gln Ser Pro Asp
 65 70 75 80

Glu Gly Val Tyr Glu Leu Ala Phe Asp Asn Ala Ser Lys Lys Val Phe
 85 90 95

Ala Ala Val Thr Asp Arg Val Asn Arg Glu Ala Asn Lys Gly Tyr Leu
 100 105 110

Tyr Ser Phe Asn Ser Asp Ser Leu Lys Val Glu Asn Lys Tyr Thr Met
 115 120 125

Pro Tyr Arg Ala Phe Ser Leu Ala Ile Asn Gln Asp Lys His Gln Leu
 130 135 140

Tyr Ile Gly His Thr Gln Ser Ala Ser Leu Arg Ile Ser Met Phe Asp
 145 150 155 160

Thr Pro Thr Gly Lys Leu Val Arg Thr Ser Asp Arg Leu Ser Phe Lys
 165 170 175

Ala Ala Asn Ala Ala Asp Ser Arg Phe Glu His Phe Arg His Met Val
 180 185 190

Tyr Ser Gln Asp Ser Asp Thr Leu Phe Val Ser Tyr Ser Asn Met Leu
 195 200 205

151

Lys Thr Ala Glu Gly Met Lys Pro Leu His Lys Leu Leu Met Leu Asp
 210 215 220

Gly Thr Thr Leu Ala Leu Lys Gly Glu Val Lys Asp Ala Tyr Lys Gly
 225 230 235 240

Thr Ala Tyr Gly Leu Thr Met Asp Glu Lys Thr Gln Lys Ile Tyr Val
 245 250 255

Gly Gly Arg Asp Tyr Ile Asn Glu Ile Asp Ala Lys Asn Gln Thr Leu
 260 265 270

Leu Arg Thr Ile Pro Leu Lys Asp Pro Arg Pro Gln Ile Thr Ser Val
 275 280 285

Gln Asn Leu Ala Val Asp Ser Ala Ser Asp Arg Ala Phe Val Val Val
 290 295 300

Phe Asp His Asp Asp Arg Ser Gly Thr Lys Asp Gly Leu Tyr Ile Phe
 305 310 315 320

Asp Leu Arg Asp Gly Lys Gln Leu Gly Tyr Val His Thr Gly Ala Gly
 325 330 335

Ala Asn Ala Val Lys Tyr Asn Pro Lys Tyr Asn Glu Leu Tyr Val Thr
 340 345 350

Asn Phe Thr Ser Gly Thr Ile Ser Val Val Asp Ala Thr Lys Tyr Ser
 355 360 365

Ile Thr Arg Glu Phe Asn Met Pro Val Tyr Pro Asn Gln Met Val Leu
 370 375 380

Ser Asp Asp Met Asp Thr Leu Tyr Ile Gly Ile Lys Glu Gly Phe Asn
 385 390 395 400

Arg Asp Trp Asp Pro Asp Val Phe Val Glu Gly Ala Lys Glu Arg Ile
 405 410 415

Leu Ser Ile Asp Leu Lys Lys Ser
 420

152

<210> 67

<211> 489

<212> DNA

<213> Escherichia coli

<400> 67

atgaaactga aagctattat attggccaacc ggtcattatta actgtattgt attttcagca 60
caggcagtgg atacgacgat tactgtgacg ggtaatgttt tgcaaagaac atgtaatgta 120
ccagggaatg tggatgtttc tttgggtaat ctgtatgtat cagactttcc caatgcagga 180
agtggatctc catgggttaa ttttgatctg tctctcaccg gatgccagaa tatgaatact 240
gttcgggcaa catttagtgg tactgcggat gggcagacat actatgcgaa tacagggaat 300
gctggcggta tcaagattga aattcaggac agggatggaa gtaatgcac atatacaaat 360
ggatatgtca agacgcttaa tgtacaaaat aataatgcaa cttttaatct taaagcccgt 420
gcagtgaata aaggccaggt tactcctgga aatatcagtt ctgttataac cgtcacctat 480
acctatgcg 489

<210> 68

<211> 2019

<212> DNA

<213> Escherichia coli

<400> 68

atgaaaatga cacggcttta tcctctggcc ttggggggat tattgctccc cgccattgct 60
aatgccccaga cttcacagca agacgaaagc acgctgggtg ttaccgccag taaacaatct 120
tcccgtctcg catcagccaa caacgtctcg tctactgttg tcagcgcgcc ggaattaagc 180
gacgcggcg tcaccgccag cgacaaaact cccagagtct tgcccgggct caatattgaa 240
aatagcggca acatgctttt ttgcagatc tcgctacgcg gcgtctcttc agcgcaggac 300
ttctataacc ccgcgtcac cctgtatgtc gatggcgtcc ctacgctttc caccaacacc 360
atccaggcgc ttaccgatgt gcaaagcgtg gagttgctgc gaggccaca gggaacgtta 420
tatggcaaaa gcgctcaggg cgggatcatc aacatcgtca cccagcagcc ggacagcacg 480
ccgcgcggct atattgaagg cggcgtcagt agccgcgaca gttatcgaag taagttcaac 540
ctgagcggcc ccattcagga tggcctgctg tacggcagcg tcaccctgtt acgccagggt 600
gatgacggcg acatgattaa cccgcgcagc ggaagcgtg acttaggcgg caccgcgcgc 660
agcataggga atgtgaaact gcgtctggcg ccggacgatc agccctggga aatgggcttt 720
gccgcctcac gcgaatgtac ccgcgccacc caggacgcct atgtgggatg gaatgatatt 780
aagggccgta agctgtcgat cagcgatggg tcaccagacc cgtacatgcg gcgctgcact 840

153

gacagccaga ccctgagtgg gaaatacacc accgatgact gggttttcaa cctgatcagc 900
 gcctggcagc agcagcatta ttccgcgcacc ttcccttccg gttcgttaat cgtcaatatg 960
 tctcagcgct ggaatcagga tgtgcaggag ctgcgcgctg caaccctggg cgatgcgcgt 1020
 accgttgata tgggtgtttgg gctgtaccgg cagaacaccc gcgagaagtt aaattcagcc 1080
 tacgacatgc cgacaatgcc ttattttaagc agtaccggct ataccaccgc tgaaacgctg 1140
 gccgcataca gtgacctgac ctggcattta accgatcggt ttgatatcgg cggcggcgctg 1200
 cgctttctcg atgataaatc cagtacacaa tatcacggca gcatgctcgg caaccctgtt 1260
 ggcgaccagg gtaagagcaa tgacgatcag gtgctcgggc agctatccgc aggtatatg 1320
 ctgaccgatg actggagagt gtatacccggt gtagcccagg gatataaacc ttccgggtac 1380
 aacatcgctc ctactgcggg tcttgatgcc aaaccgttcg tcgccgagaa atccatcaac 1440
 tatgaacttg gcaccgcgta cgaaaccgct gacgtcacgc tgcaagccgc gacgttttat 1500
 acccacacca aagacatgca gctttactct ggcccggctg ggatgcagac attaaagcaat 1560
 gcgggtaaag ccgacgccac cggcggttgag cttgaagcga agtggcggtt tgcgccaggc 1620
 tggtcacggg atatcaatgg caacgtgatc cgttccgaat tcaccaatga cagtgagttg 1680
 tatcacggta accgggtgcc gttcgtacca cgttatggcg cgggaagcag cgtgaacggc 1740
 gtgattgata cgcgctatgg cgcactgatg ccccgactgg cggttaatct ggtcgggccg 1800
 cattatctcg atggcgacaa ccagttgcgg caaggcacct atgccaccct ggacagcagc 1860
 ctgggctggc aggcgactga acggatgaac atttccgtct atgtcgataa cctgttcgac 1920
 cgtcgttacc gtacctatgg ctacatgaac ggcagcagcg ccgtcgcgca ggtcaatatg 1980
 ggtcgcaccg tcggtatcaa tacgcgaatt gatttcttc 2019

<210> 69

<211> 738

<212> DNA

<213> Escherichia coli

<400> 69

atgaataagg tttttgttgt ttcagtgggt gccgcagcct gtgtatttgc agtaaatgca 60
 ggagcaaagg aaggtaaaag cggtttttat ctgaccggta aagccggtgc ctctgtgatg 120
 tcactttcag accagcggtt cctgtcagga gatgaggaag aaacatcaaa gtataaaggc 180
 ggcgatgacc atgatacggg attcagtggc ggtattgcgg tcggttatga tttttatccg 240
 cagttcagta ttccggttcg tacagaactg gagttttacg ctcgaggaaa agctgattcg 300
 aagtataacg tagataaaga cagctgggtca ggtgggtact ggcgtgatga cctgaagaat 360

154

gaggtgtcag tcaacacact aatgctgaat gcgtactatg acttccggaa tgacagcgca 420
 ttcacaccat gggatatccgc agggattggc tacgccagaa ttcaccagaa aacaaccggt 480
 atcagtacct gggattatga gtacggaagc agtggtcgcg aatcgttgtc acgttcaggc 540
 tctgctgaca acttcgcatg gagccttggc gcgggtgtcc gctatgacgt aaccccggat 600
 atcgctctgg acctcagcta tcgctatctt gatgcagggtg acagcagtgt gagttacaag 660
 gacgagtggg gcgataaata taagtcagaa gttgatgtta aaagtcatga catcatgctt 720
 ggtatgactt ataacttc 738

<210> 70

<211> 498

<212> DNA

<213> Escherichia coli

<400> 70

atgaaactga aagctattat attggccacc ggtcttatta actgtattgc attttcagca 60
 caggcagtgg atacgacgat tactgttaca gggagggtat tgccacgtac ctgtaccatt 120
 ggtaatggag gaaacccaaa cgccaccgtt gttttggata acgcttacac ttctgacctg 180
 atagcagcca acagcacctc tcagtggaaa aatttttcgt tgacattgac gaattgtcag 240
 aatgtaaaca atgttacttc atttgggtgga accgcagaaa atacaaatta ttacagaaat 300
 acaggggatg ctactaatat catgggttgag ctacaggaac aaggtaatgg taataccccc 360
 ttgaaagttg gttcaacaaa agttgttaca gtgagcaatg ggcaggcgac attcaatctt 420
 aaagtccgtg ccgtaagcaa aggtaatgct ggtgcgggaa gtattaattc acaaattact 480
 gtcacctata cctatgcg 498

<210> 71

<211> 3885

<212> DNA

<213> Escherichia coli

<400> 71

atgaataaaa tatactccct taaatatagt gctgccactg gcggactcat tgctgtttct 60
 gaattagcga aaagagtttc tggtaaaaca aaccgaaaac ttgtagcaac aatgttgtct 120
 ctggctgttg ccggtacagt aaatgcagca aatattgata tatcaaatgt atgggcgaga 180
 gactatcttg atcttgcaaa aaataaagggt attttccagc ccggagcaac agacgtaaca 240
 atcactttaa aaaacggaga taaattctct ttocataatc totcaattcc ggatttttct 300
 ggtgcagcag cgagtggcgc agctaccgca ataggagggtt cttatagtgt tactgttgca 360

cataacaaaa agaaccctca ggccgcagaa acccaggttt acgctcagtc ttcttacagg	420
gttggttgaca gaagaaattc caatgatttt gagattcaga ggtaaataa atttgttggtg	480
gaaacagtag gtgccacccc ggcagagacc aaccctacaa catattctga tgcattagaa	540
cgctacggta tagtcacttc tgacggttca aaaaaaatca taggttttcg tgctggctct	600
ggaggaacat catttattaa tggatgaatcc aaaatctcaa caaattcagc atatagccat	660
gatctgttaa gtgctagtct atttgaggtc acccaatggg actcatcagg catgatgatt	720
tataaaaatg ataaaacatt tcgtaatctt gaaatattcg gagacagcgg ctctggagca	780
tacttatatg ataacaaact agaaaaatgg gtattagtcg gaacaacca tggatttgcc	840
agcgttaatg gtgaccaact gacatggata acaaaataca atgataaact ggtagtgag	900
ttaaagata cctatagtca taaaataaat ctgaatggca ataatgtaac cattaaaaac	960
acagatataa cattacacca aaacaatgca gataccactg gtactcaaga aaaaataact	1020
aaagacaaag atattgtgtt cacaaatggg ggagatgtcc tgtttaagga taatttggat	1080
tttggttagcg gtggtattat ctttgacgaa ggccatgaat ataacataaa cggtcaggga	1140
tttacattta aaggagcagg aattgatatc ggaaaagaaa gcattgtaaa ctggaatgca	1200
ttgtattcca gtgatgatgt ttacacaaa ataggccccg gtactctgaa tgttcaaaaa	1260
aaacaggggg caaatataaa gataggtgaa ggaaatgtta ttcttaatga agaaggaaca	1320
tttaacaata tataccttgc aagcggaaat ggtaaggtaa tactaaataa agataattcc	1380
cttggcaatg atcaatatgc ggggatattt ttactaaac gtggtggtac gctagattta	1440
aatggacaca atcagacttt tactagaatt gccgccactg acgatggaac aacaataact	1500
aactcagata caacgaaaga agcgttctg gcaatcaata acgaagactc ctacatatat	1560
catgggaaca taaatggcaa tataaaacta acgcacaata ttaattctca ggataagaaa	1620
actaatgcaa aattaattct ggatggtagt gtaaacacaa aaaatgatgt tgaagtcagt	1680
aatgccagtc ttaccatgca aggccatgca acagagcatg caatattcag aagctcagcg	1740
aatcattgct ccctggtatt tctttgtgga acggactggg tcaccgtttt gaaagaaaca	1800
gagagttcat ataataaaaa attcaattct gattacaaaa gtaataatca gcagacctca	1860
tttgatcagc ctgactggaa aaccggggtg tttaaatttg atacattaca cctgaacaat	1920
gctgactttt caatatcacg caatgccaat gttgaaggaa atatatcagc aaataaatca	1980
gctatcacaa tcggcgataa aaatgtttac attgataatc ttgcagggaa aaatattact	2040
aataatggtt ttgacttcaa acaaaactatc agtactaatc tatccatagg agaaactaaa	2100

tttacagggtg gcatcactgc acataacagc caaatagcca taggtgatca agctgtagtt 2160
acacttaatg gtgcaacctt tctggataat actcctataa gtatagataa aggagcaaaa 2220
gttatagcac aaaattccat gttcacaaca aaaggatttg atatctccgg tgaactgact 2280
atgatgggaa tccctgaaca gaatagtaaa actgtaacgc cgggtctcca ctacgctgct 2340
gatggattca ggctgagtgg tggaaatgca aatttcattg ccagaaatat ggcatctgtc 2400
accggaaaata tttatgctga tgatgcagca accattactc tgggacagcc tgaaactgaa 2460
acaccgacta tatcgtctgc ttatcaggca tgggcagaga ctcttttgta tggctttgat 2520
accgcttadc gaggcgcaat aacagccccc aaagctacag ttagcatgaa taatgcgac 2580
tggcatctaa atagccagtc atcaattaat cgtctagaaa caaaagacag tatgggtcgt 2640
tttactgggtg ataatgggaa gtttacaacc cttacagtga acaaccttac tatagatgac 2700
agtgcatttg tgctgcgtgc aaatctggcc caagcagatc agcttggtgt caataaatcg 2760
ttgtctggta aaaacaacct tctgttagtc gacttcattg agaaaaatgg aaacagcaac 2820
ggactgaata tcgatctggc cagcgcacca aaaggaactg cagtagatgt ctttaaagct 2880
acgactcgga gtattggctt cagtgatgta acaccgggta tcgagcaaaa gaacgatata 2940
gacaaagcaa catggactct gatcggctat aaatctgtgg ccaacgccga tgcgggctaaa 3000
aaggcaacat tactgatgtc aggcggctat aaagccttcc ttgctgaggt caacaacctt 3060
aacaaacgta tgggtgatct gcgtgacatt aacggtgagt ccggtgcatg ggcccgaatc 3120
attagcggaa ccgggtctgc cggcgggtgga ttcagtgaac actacacca cgttcaggctc 3180
gggtcgggata acaaacatga actcgatggc cttgacctct tcaccggggg gaccatgacc 3240
tataccgaca gccatgcagg cagtgatgcc ttcagtgggtg aaacgaagtc tgtgggtgcc 3300
gggtctctatg cctctgccat gtttgagtcc ggagcatata tcgacctcat cggttaagtac 3360
gttcaccatg acaacgagta taccgcaact ttccgccggc ttggcaccag agactacagc 3420
tcccactcct ggtatgccgg tgcggaagtc gggtaccgtt accatgtaac tgactctgca 3480
tggattgagc cgcaggcgga acttgtttac ggtgctgtat ccgggaaaca gttctcctgg 3540
aaggaccagg gaatgaacct caccatgaag gataaggact ttaatccgct gattgggcgt 3600
acogggtgttg atgtgggtaa atccttctcc ggtaaggact ggaaagtcac agcccgcgcc 3660
ggccttggct accagtttga cctgtttgcc aacggtgaaa ccgtactgcg tgatgcgtcc 3720
ggtgagaaac gtatcaaagg tgaaaaagac ggctcgtatgc tcatgaatgt tggctctaac 3780

gcccgaattc gcgataatct tcgcttcggt cttgagtttg agaaatcggc atttggtaaa 3840
 tacaacgtgg ataacgcgat caacgccaac ttccgttact ctttc 3885

<210> 72

<211> 426

<212> DNA

<213> Escherichia coli

<400> 72

atgattaata ttcccagtc caccgctggt gttatggcgc tggtagccat cagcacgctt 60
 cccagcccta gcagggtaaa gcttatgcc a taccctcca gagcccacaa caccacaggt 120
 ttactgccag tacgggaaat ttgctttccc caccacgggg acgatggcag aaacagcatt 180
 gagccaagca tcagcagggc agcccataca gacagactca gatttgtctg tatgaccaga 240
 acagggagca caaccagcag accgttctgc ccgataccga gaagcccggc actgaacgca 300
 agtggccagc aggacagtgg tttttggggc gtatcttcga tcccagggtga cattttaatg 360
 tttcaactcc atgtattaat tgtgtttatt tgtaaaatta atttatctga caataacatt 420
 tcttat 426

<210> 73

<211> 954

<212> DNA

<213> Escherichia coli

<400> 73

atgtatgcc gcgagtatcg ctcaacacgc ccgcataaag cgattttctt tcattttctt 60
 tgccctaccc ttatctgtag tgcgcaagtt tatgcgaagc cggatatgcg gccactgggg 120
 ccgaatatag ccgataaagg ctccgtgttt taccatttca gcgccacctc ttccgactct 180
 gtcgatggca cagccatta tcgggtatgg acggccgtgc cgaatacaac cgcaccggca 240
 tcgggttacc cgattttata tatgcttgac ggtaacgcag ttatggaccg cctggatgac 300
 gaactgctca aacaattgtc agaaaaaaca ccgccagtga tcgtggctgt cgggtatcag 360
 accaacctcc ctttcgatct caacagcagg gcttacgact atacgccagc agcagaaagc 420
 agaaaaacag atctccactc agggcggttt agccgtaaga gtggtggcag caacaacttc 480
 cgccagttac tggaaacgcg tattgcccc aaagtggaac agggactgaa tatcgatcgg 540
 caacgcgcgc gcttatgggg gcaactcctac ggcgccctct tcgtgctgga ttctggctg 600
 tctctctctt acttcgggtc gtactacagc gccagccgt cgttgggcag aggttatgat 660
 gctttgctaa gccgcgttac ggcggttgag cctctgcaat tctgcaccaa acacctggcg 720
 ataatggaag gctcggcgac acaggggtgat aaccgggaaa cgcattgctgt cggggtgctg 780

158

togaaaattc ataccaccct cactatactg aaagataaag gcgtcaatgc cgtatatttg 840
 gatttcccca acctgggaca cgggccgatg ttcaatgcct cctttcgcca ggcactgtta 900
 gatatcagtg gtgaaaacgc aaattacaca gcagggtgtc atgagttaag ccac 954

<210> 74

<211> 2175

<212> DNA

<213> Escherichia coli

<400> 74

atgagaatta acaaaatcct ctggctgcta actgtgctcc tagttgggtt gaatagccag 60
 gtatcagtag ccaaatactc cgacgatgat aatgacgaga ctctgggtgtt ggaagccacc 120
 gctgagcagg tattaaaaca gcagccgggc gtgtcgggtta ttaccagcga ggatattaaa 180
 aagacccttc cggtaaacga cctttcagat attattcgta aaatgcctgg tgttaatctt 240
 accggcaata gcgcctcggg cacacgcggg aataaccgcc agatcgatat tcgtgggtatg 300
 gggccggaaa acaccttaat tttaattgat ggtgtaccgg tgacgtcacg taactccgtg 360
 cgttatagct ggcggtggga gcgtgatacc cgcggtgaca ccaactgggt gccaccggaa 420
 caggttgagc gtattgaagt gatccgcggc cctgcggcgg cgcgctacgg ttcggggggc 480
 gccggggggg tggatgaacat cattaccaa cgteccacca acgactggca cggttcgctg 540
 tcgttataca ccaaccagcc ggaaagtagc gaagagggcg ctacgcgtcg cgccaatttc 600
 agccttagtg ggctctcggc tggatgatgt cttaccacgc gtttgtatgg taacctgaat 660
 aaaacggatg ctgacagttg ggatattaat tctccggctg gtacgaaaaa cgcagccggg 720
 catgaagggg tacgtaacaa agatattaac ggcgttgtct cgtggaaatt aaatccgcag 780
 cagattctcg atttcgaagt cggatatagc cgccagggga atatctatgc gggcgatacg 840
 cagaacagtt cttccagtgc agttaccgaa agcctggcaa aatccggcaa agagacgaac 900
 cgctgtgacc gacagaatta tggcattacg cataatggta tctgggactg gggacaaagt 960
 cgctttgggtg ttattacga gaaaaccaat aatacccgca tgaatgaagg attatccggc 1020
 ggtggtgaag gacgtatatt agcgggtgaa aagtttacga ccaatcgct gagttcctgg 1080
 cgaaccagcg gtgagcttaa tattcctttg aatgtgatgg ttgatcaaac gctgaccgtt 1140
 ggtgcagagt ggaaccgca taagctcgat gatccttcct ctaccagcct gacggtgaat 1200
 gacagagata tcagcgggat ttctggctct gctgcggatc gcagcagtaa aaatcattct 1260
 caaatcagtg cgctgtatat tgaagataac attgagccgg ttcctggcac gaatatcatt 1320

159

ccgggctgc gctttgatta tctcagcgac tccggcgga acttcagccc cagtctgaat 1380
 ctttcgcagg aattgggcca ttatttcaaa gtcaaagcag gggttgccc aacctttaaa 1440
 gccccaaacc tgtatcaatc cagtgaaggg tatctgctct actcgaaagg caatggctgt 1500
 ccaaaagata ttacatcagg cgggtgctac ctgatcggtataaaagatct cgatccggaa 1560
 atcagcgta ataaagaaat tggactggag ttcacctggg aagattacca cgcaagtgtg 1620
 acctacttcc gcaatgatta ccagaataag atcgtggccg gggataacgt tatcgggcaa 1680
 accgcttcag gcgcataatat cctcaagtgg cagaatggcg ggaaagctct ggtggacggt 1740
 atogaagcca gtatgtcttt cccactgggtg aaagagcgta tgaactggaa taccaatgcc 1800
 acatggatga tcacttcgga gcaaaaagac accggtaatc ctctgtcgggt catcccgaaa 1860
 tatactatca ataactcgct taactggacc atcaccagcag cgttttctgc cagcttcaac 1920
 tggacgttat atggcagaca aaaaccgct actcatgcgg aaaccgcag tgaagatact 1980
 ggcggtctgt caggtaaaga gctggcgct tattcactgg tggggacgaa cttcaattac 2040
 gatattaata aaaatctgcg tcttaatgtc ggcgtcagta atatcctcaa taaacagatc 2100
 ttccgatctt ctgaaggggc gaatacctat aacgagccag gccgggctta ttatgccgga 2160
 gttaccgcat cattc 2175

<210> 75

<211> 3042

<212> DNA

<213> Escherichia coli

<400> 75

atgggtaacc aatggcaaca aaaatatctt cttgagtaca atgagttgggt atcaaatttc 60
 ccttcacctg aaagagttgt cagcgattac attaagaatt gttttaaaac tgacttgccg 120
 tggtttagtc ggattgatcc tgataatgct tatttcatct gcttttctca aaaccggagt 180
 aatagcagat cttatactgg atgggatcat cttgggaaat ataaaacaga agtactgaca 240
 ctcaactcaag ccgctcttat taatattgggt tatcgttttg atgtttttga tgatgcaaat 300
 tcaagcacag gaatttataa acaaaagagt gcagatgtgt ttaacgaaga aaatgaagaa 360
 aaaatgctcc cgtcgggaata cctgcatttt ttacaaaagt gtgattttgc aggtgtttat 420
 ggaaaaactc tgtcagatta ctggtcgaaa tactatgata aatttaagct ttactaaaa 480
 aattattata tttcttctgc tttgtatctt tataaaaatg gagagcttga tgagcgtgaa 540
 tataatttct ccatgaacgc cttaaatacgc agtgataata tatcactatt attctttgat 600
 atttatggat attacgcac tgatattttt gtagccaaaa ataatagataa ggtaatgctt 660

ttcattcctg gtgcaaaaaa acctttttta ttcaagaaga atatcgctga tttgcggctt	720
acccttaaag aacttattaa ggatagtgac aacaaacaat tactttccca acatttttca	780
ttatatagtc gtcaagatgg agtttcctat gcaggagtaa attctgttct acatgcaata	840
gaaaatgatg gtaattttta tgagtcttac tttctgtatt ccaataagac acttagcaat	900
aaagatgttt ttgatgctat agctatttct gttaagaaac gcagtttcag tgatggtgat	960
atcgttataa aatcaaacag tgaagctcaa cgagactatg ctctgactat actccagacg	1020
attttatcaa tgaccctat atttgatctc gtagtcccg aggtatctgt tccgcttgga	1080
ctggggatta ttacttccag tatggggatc agttttgatc aactgattaa tgggtgatact	1140
tatgaagaac gtcgttctgc tatacctggg ttggcgacaa atgcagtatt gcttggtctg	1200
tcttttgcaa ttccactctt gattagtaag gcaggaataa accaggaggt acttagcagc	1260
gttataaata atgagggcag gactctgaat gaaacaaata tcgatatatt tttgaaggaa	1320
tatggaattg ctgaagatag tatatcctca actaatttgt tagacgttaa gcttaaaagt	1380
tccgggcagc atgtcaatat tgtaaagctt agtgatgaag ataatacaat tgtcgctgta	1440
aaaggaggtt ctctgagcgg catctactat gaagtggaca ttgaaacagg atatgagatt	1500
ttatcccgaa gaatttatcg taccgaatat aataatgaaa ttctctggac tcgaggtggt	1560
ggtctaaaag gggggcagcc atttgatttt gaaagtctca atattcctgt atttttttaa	1620
gatgaacctt attctgcagt gaccggatct ccgttatcat ttattaatga tgacagctca	1680
cttttatatc ctgatacaaa cccaaaatta ccgcaaccaa cgtcagaaat ggatattgtt	1740
aattatgtta agggttctgg aagctttggg gatagatttg taactttgat gagaggagct	1800
actgaggaag aagcatggaa tattgcctct tatcatcagg ctgggggaag tacagaagaa	1860
ttacacgaaa ttttgttagg tcagggccca cagtcaagct taggttttac tgaatatacc	1920
tcaaatgtta acagtgcaga tgcagcaagc agacgacact ttctggtagt tataaaagtg	1980
cacgtaaaat atatcaccaa taataatgtt tcatatgtta atcattgggc aattcctgat	2040
gaagccccgg ttgaagtact ggctgtgggt gacaggagat ttaattttcc tgagccatca	2100
acgcctcctg atatatcaac catacgtaaa ttgttatctc tacgatattt taaagaaagt	2160
atcgaaagca cctccaaatc taactttcag aaattaagtc gcgtaatat tgatgtgctt	2220
aaaggacggg gaagtatttc atcgacacgt cagcgtgcaa tctatccgta ttttgaagcc	2280
gctaattgctg atgagcaaca acctctcttt ttctacatca aaaaagatcg ctttgataac	2340

161

catggctatg atcagtatct ctatgataat acagtggggc taaatgggtat tccaacattg 2400
 aacacctata ctggggaaat tccatcagac tcatcttcac tcgggtcaac ttattggaag 2460
 aagtataatc ttactaatga aacaagcata attcgtgtgt caaattctgc tcgtggggcg 2520
 aatggtatta aaatagcact tgaggaagtc caggagggta aaccagtaat cattacaagc 2580
 ggaaatctaa gtggttgtag gacaattgtt gcccgaaaag aaggatatat ttataaggta 2640
 catactggta caacaaaatc tttggctgga tttaccagta ctaccggggg gaaaaaagca 2700
 gttgaagtac ttgagctact tacaaaagaa ccaatacctc gcgtggaggg aataatgagc 2760
 aatgatttct tagtcgatta tctgtcggaa aattttgaag attcattaat aacttactca 2820
 tcatctgaaa aaaaaccaga tagtcaaatc actattatct gtgataatgt ttctgttttc 2880
 ccttacttcc ttgataatat acctgaacat ggctttggta catcggcgac tgtactgggtg 2940
 agagtggacg gcaatgttgt cgtaaggctc ctgtctgaga gttattctct gaatgcagat 3000
 gcctccgaaa tatcggtatt gaaggtattt tcaaaaaaat tt 3042

<210> 76

<211> 1362

<212> DNA

<213> Escherichia coli

<400> 76

atgggtggaca tgattaatga aagtgcacgg caaacgccag tcattgcaca aacggacgtt 60
 ctggttatcg ggggcggtcc ggcaggatta tccgctgcc a ttgcggcagg gcggttaggt 120
 gccagaacca tgattgttga gcgctacggg tcgctaggcg gcgtattgac gcaggtcggg 180
 gtagaaaagt ttgcctggta tcgtcatccg gggacggaag attgtgaagg gatctgtcgt 240
 gagtatgaag gccgcgcacg agcgtctgggt ttcacacgac cagaacctca gtcaattagc 300
 gaagttatag atactgaagg atttaaagt gtcgcgcgac agatgattac ggaatctggc 360
 gttgagccgt tatatcactc ctgggttgtg gacgtgatca aggacgggga tacgttatgc 420
 ggtgttatcg tcgagaataa atcaggtcga ggggcaattc tggcgaaaag aatcgtcgat 480
 tgcacggggg atgctgatat tgccgctcgt gcaggcgcgc cctggacgaa acggagcaag 540
 gaccaactga tgggcgtcac cgtgatgttc agttgcgcag gtgttgatgt ggcacgcttt 600
 aaccgttttg ttgcggaaga acttaagccg acctacgcgg attggggcaa aaactggacg 660
 attcaaacca cgggtaaaga agaccgatg tttagcccg atatggagga tatttttacc 720
 cgcgcgcaac aggatgggtg gattocaggt gacgcccagg cgattgccgg aacctggctg 780
 accttttctg aaagcgggtga ggctttccag atgaatatgg tgtacgcctt tggttttgac 840

tgtaccgatg tcttcgattt aaccaaagct gagattgccg gaaggcagca agcattatgg 900
 gcaattgacg cactacgcca ctatgttccg ggctttgaaa atgtacgggtt acgcaatttt 960
 ggtgccacgc tggggacgcg tgaatcacgg cttattgagg gggaaatacg tattgctgat 1020
 gattacgtcc ttaatcaggg gcgttggtcg gacagtgtag ggattttccc ggaatttatt 1080
 gatgggtccg gttatctcat ttgccaacg accgggcgtt tctttcagat cccttatggg 1140
 tgtctgggtc cgcaaaaagt ggagaacctt ttggtgcgcg gtcgctgtat ttccgcaggc 1200
 gtagttgcac atacttctat gcgtaacatg atgtgttgtg ccgttacggg tgaggccgca 1260
 ggtactgccg ccgtgggttc gctacagcaa aattgcaccg tgcgtcaggt tgctatccct 1320
 gatttgcaaa acacgctgca acagcagggc gttcgtctgg ca 1362

<210> 77

<211> 759

<212> DNA

<213> Escherichia coli

<400> 77

atgtctgcc aagacgact tcttattgcg tgtacottga taacagctat ctatcatttt 60
 cctgcatatt cttcattaga atataaagga acctttgggt caataaatgc gggttatgca 120
 gactggaaca gtggatttgt aaacactcac cgtggtgaag tatggaaagt gactgcggat 180
 tttggggtaa attttaaaga agcagaattt tactcatttt atgaaagtaa tgtactcaat 240
 catgctgtag caggagagaaa tcatacgggt tcagcaatga cgcgtgtcag actctttgac 300
 tctgatatga cattctttgg caaaatttat ggccaatggg ataactcatg gggtgacgat 360
 ctggacatgt tttatggatt cggttacctc ggctggaacg gcgagtgggg cttttttaaa 420
 ccgtatattg gattgcataa tcaatctggg gactacgtat cagctaaata tggcacaacg 480
 aatggttgga atggttatgt tggtggctgg acagcagtat taccatttac gttatttgac 540
 gaaaaatttg ttttatctaa ctggaatgaa atagaactgg acaggaacga tgcttacacg 600
 gagcagcaat ttggccggaa cgggttaaat ggcggtttaa ctattgctg gaagttctat 660
 cctcgtctga aagcaagtgt gacgtggcgt tatttcgata ataagctggg ctacgatggc 720
 tttggcgatc aaatgattta tatgcttggt tatgatttc 759

<210> 78

<211> 1476

<212> DNA

<213> Escherichia coli

<400> 78

163

```

atggccagtt tgatcggcct tgcagtttgc acaggggaatg ctttttagtcc tgccttagcc      60
gcagaggcta aacaaccta ttagtgcatt attatggcgg atgatttagg ttatggcgat      120
ttagcaacat atggtcatca gatcggttaa acacctaata tcgacaggct tgcccaggaa      180
ggggtcaaat ttactgacta ctatgcccc gctcctttta gttcaccttc acgcgcaggg      240
ctattaaccg gccggatgcc atttcgtact ggaattcgct catggattcc ttcaggcaaa      300
gatgttgctt tagggcgtaa cgaactcacg attgctaata tactcaaagc gcaagggtac      360
gacacggcaa tgatgggtaa gctgcatctg aatgcaggcg gcgatcgac cgatcagcca      420
caagcacaag atatgggctt tgattactca ctggctaata cggcgggctt tgttaccgac      480
gccacgctgg ataacgctaa agaacgccc cgttatggca tggtttacc gacaggctgg      540
ctacgtaatg ggcaaccac tccacgagcc gataaaatga gcggtgagta tgtcagttcg      600
gaagtcgtca actggctgga taacaaaaag gacagcaagc ctttcttct ctatgttgct      660
tttaccgaag tgcataagcc cctggcttcg cccaaaaaat acctcgacat gtactcacia      720
tatatgagcg cgtatcagaa gcagcatcct gatttatatt atggcgactg ggcagacaaa      780
ccctggcgtg gtgtggggga atattatgcc aatatcagct atctggatgc acaggttgga      840
aaagtgcctg ataaaatcaa agcgatgggt gaagaagata acacaatcgt tatttttacc      900
agtgataacg gtccggtaac gcgtgaagcg cgaaagtgt atgagctgaa tttggcaggg      960
gaaacggatg gattaacggc tcgcaaggat aacctttggg aaggcggaat tcgtgttcca     1020
gccattatta aatatggtaa acatctacca cagggaatgg tttcagatac acccgtttat     1080
ggctctggact ggatgcctac tttagcgaaa atgatgaact tcaaattacc tacagaccgt     1140
actttcgatg gtgaatcgct ggttcctggt cttgagcaaa aagcattgaa acgcgaaaag     1200
ccattaatth tcgggattga tatgccattc caggatgatc caaccgatga atgggcgatc     1260
cgtgatggtg actggaagat gattatcgat cgcaataata aaccgaaata tctctacaat     1320
ctgaaatctg atcgttatga aacacttaat ctgatcggtg aaaaaccaga tattgaaaaa     1380
cagatgtatg gtaagttttt aaaatataaa actgatattg ataatgattc tctaataaaa     1440
gccagaggtg ataaaccaga agcggtgacc tggggc                                1476

```

<210> 79

<211> 954

<212> DNA

<213> Escherichia coli

<400> 79

```

gtgacaacaa ctatctgcgc tatgggcgaa ttgctggccg agtttttgtc ccgcaaccca      60

```

164

catcaaaaat tcaactcagcc tggggagttt atcggggccat ttcccagcgg tgcgccagca 120
 atttttgctg ctcaggtggc aaaactgtcc catcggggcca tcttctttgg atgtgttggt 180
 aatgatgatt ttgcccgact cattatagag cgtctccgtc atgaagggtg cattaccgat 240
 gggatccatg ttatgaacaa tgccgtcaca ggtacggcgt tcgtgagtta tcaaaatccc 300
 cagcagcggg atttcgtctt taatatccct aacagcgcct gcggtttggt tactgccgag 360
 cacattgata aggatctgct taaacagtgt aaccatctgc atattgtggg ctcacgttg 420
 ttctcatttc gcatgatcga tgtcatgcgt aaagcaataa cgacgatcaa atcggtggc 480
 ggcaccgttt ctttcgatcc caatattcgc aaagagatgc tgagcattcc tgaaatggcg 540
 caggctctcg attatttgat tgaatatacg gatattttta tcccagcga aagcgaactc 600
 cttttcttcg cgcgtcacia aaatctgtca gaggaacaga ttgttagcga tcttctccac 660
 gggggcgtaa aacatgtggc gataaaacgc gccagcgtg gggccagcta ttacaagctt 720
 aaaaacggta cattacacgc ccagcatggt gcaggtcacg atatcgaaat tatcgatcca 780
 acgggtgcag gcgactgctt tggcgcaacg tttatcactc ttttcttate cggtttcccg 840
 gcacacaagg cgctgcaata tgcaaatgcc agcggcgcgc tcgcccgaat gcggcaagg 900
 ccgatggaag ggatatcctc actggcagac attgaagact ttttgcagca gcac 954

<210> 80

<211> 513

<212> DNA

<213> Escherichia coli

<400> 80

atgaagatat tcattagttt atttttgttt ataatatcaa caaattcttt tgctgatgat 60
 atcactcatg ccggagtggg tcgtattgaa gggttaatta ccgaaaaaac ctgcattatt 120
 tctgatgagt caaaaaattt tacagttaat atgccagacg taccagtag ttcggtaagg 180
 agtgcagggg atgttactga aaaggtttat ttttccataa cgtaaccgg ctgtggtagt 240
 gatgttggca acgcgtatat aaagtacc ggcaatacag tttctgaaga tgccagttta 300
 tataagctgg aagatggctc ggtagagggg cttgcactta cgatttttga taagaacaaa 360
 ggcagtatta gtaatgatgt taaaagcatg gttttttcac ttacatcatc agttgataat 420
 atattgcatt tttttgcggc ttacaaagca ttaaaaaata atgtccaacc aggggatgca 480
 aatgcgtcag tatcgtttat tgtcacctat gat 513

<210> 81

165

<211> 603
 <212> DNA
 <213> Escherichia coli
 <400> 81
 atgattaaat tccggcttta tattccccct gtaattctcg gttttgttat cgtaccatta 60
 ttggtatggc cgacgggttat tgccttagcc gtacttatat tcacgttaac ttttctggcg 120
 gaaataatat tctcctttcc gtccttggtt gtgcgtatct ctcttcagga attacaactt 180
 gagttattgg ttgtatatgc actttttttc agtgtaatgg gtggcatcgg ttggcaattc 240
 tcccgagaa cgcctcctga attaaaaaac aggcacatt gctggctggc cttttctccg 300
 gtctatttct ggttaattct ctgaatttc attctttata tttctccaga gaaatcagcg 360
 ttgctggaaa atatccgaaa tttctttctg acatttgtct ggcttcccc gaatttttcc 420
 ctttttggc cgcagccgtg gactgatttt gtcggccoga ttagtgocca gcttggtttt 480
 gcgttgggat attattgcca gtggcgtagc aaaaatagaa gccataggaa gaagtggggc 540
 gattgggtaa cgtgcttaag tttggcgatt ttagctctgg ggccgttatt caattattta 600
 caa 603

<210> 82
 <211> 702
 <212> DNA
 <213> Escherichia coli
 <400> 82
 atgaaattca atttatctaa tttatccgca gtattactgg catcaggat gctgatgtct 60
 actgcggtaa ccgcagcacc cggcgatgca acacaatttg gtggggcgga tactgactgg 120
 agcaccgttg attatcccag gctcactgat atggatgaca acgttgattc aatggggggg 180
 aaaatccgct ttactggccg tgtagtgaag gctacctgta aggtcgcaac cgattcaaaa 240
 cagattgaag ttgtcctgcc ggttgtgctt tccaaccttt tcaactggtat cgacgtagaa 300
 gcacaggggg cgagcaacca gaccgatttc aatattaatc tgaccgaatg tagcaatata 360
 gatgatcaga aaattgagtt ccgtttttacc ggtactgcag atagcgctaa taaaacgctc 420
 gctaacgaag tagaaggatc aacggatgct gacaacagcg gcaatgcggg ggcgactggt 480
 gtagggattc gaatttactc caaaggtagc acgaataatg gtctgattaa cctgaatacc 540
 actgcggcag agggtagcgc ctccaccgcc gcttatacaa ttccaggaaa tgctacgacc 600
 catgatttca gcgcggcctt tactgcaggt tatgctcaaa acggtagcac tgttgacca 660
 ggtgtagtta agtcaacagc aagttttggt gtgctgtacg ag 702

<210> 83
 <211> 1008
 <212> DNA
 <213> Escherichia coli
 <400> 83
 atgcgtatac atacttattg gtatagaaga tatttcattt tattgattat tatattttca 60
 aatgttcttt cttctattgc taatgctgaa gatatggggc gagaacgtgc atattgttat 120
 ccgggttcac cgagtaataa tactacgcct gcaccccttt cttataattt tgggtactata 180
 gtgggtttctg atgtcaacaa aaatgcgcct ggcaactgtat tgccatcaca aatctggaag 240
 gttggaacct ataaggctta ttgtaattct cttgatgatt atgaaattta cttcagtgtc 300
 gtctctggaa tagatccgtc tgggtgccagt ggtgatcatc aagggagtga tgtattttatt 360
 ccactcacc atgaaatata tgtctctact catataaaac ttataaatca aaatggcaca 420
 atgacagata aaattgtgcc attcgaaaat tataatacca attatccggg ggacagaagc 480
 aaaccatcta attgggcata aggtactgaa ggatatatta aaatcaggat tgataaaaaa 540
 attatatctg atgtttcatt aagtaacgta ttattggtgt cattatatgt cagccagatc 600
 cctaccgaac atggctctat ccctgtcttt aatgcctaca taggaaactt aaatattcag 660
 gttccgcaag gttgcactat taatgagggc acgagtttta ctgttaatat gccggatgtg 720
 tggggcagtg aattgagccg ggctgggtgcc ggagcgaagc ccgctgggtg tactcctgta 780
 gcaacaacta ttccgattaa ttgtacgaat aaagatacag atgcggtaat gacgttggtta 840
 ttgcacggta acatttccgc cacacgtgat accaatggga aacaaagtat tattcaggca 900
 caagataatc ctgatgttgg tattatgatt atggatagtc agcaaaactc cgtagattta 960
 aatgccttgg caacatcagt aggcgttccg ttcagattgg tggaaaac 1008

<210> 84
 <211> 2592
 <212> DNA
 <213> Escherichia coli
 <400> 84
 atgaacctaa agctcaaaag atgcgaatat tggatggcgg cacaaaagca gatgaaacgg 60
 gttgtgccgc ttcttctggg tattatgcct gcattgtcaa tcgcgggaat gcgctttaac 120
 cctgcttttc tgcgggtga tactgaagct gttgctgaat tatcccgctt cgagaaaggg 180
 atgacttata ttcttggtag ctatgaagtc gaagtttggg tcaatgattc ccctttactc 240
 tctcgactg taacttttaa agcagacgat gagaatcaac tgattccctg cctttcactt 300
 gctgacttat taagccttgg aattaacaaa aatgcgctgc cagagcaggc tttggcttca 360

tctgaaaata gttgccttga tttgcgtatc tggtttcccg atgtgcatta catgccggag	420
ctggatgcac agagacttaa actgaccttt ccacaggcga taataaaacg tgacgctcgc	480
ggatatattc caccagaaca gtgggataac ggtattacag cttttttgct gaattatgac	540
ttttctggta ataacgatcg tggtgattac ttttcaaata actattatth aaatcttcgc	600
gctgggatca atattggtgc atggcgthtt cgcgattatt caacctggag tctgaggagt	660
aattcagcag gtaaaactgga gcatatcagt agtacgttgc agcgcgthtat ttttctttc	720
agaagtgaat taacgctagg agatacatgg tcatcatcag atgttttcga cagtgttagt	780
attcgtggca taaaactgga atctgacgaa aatatgttgc ccgatagtc aagtggthtc	840
gctccacagg tgcgcggaat tgcgaaaagt cgcgctcagg taacaatcaa acagaatggt	900
tatgtcatth atcaaaccta tatgccgccg ggacctttg agattagcga tottaacctg	960
acatcatctg cgggagatct ggaagttacc atcaaagagt ctgataatth agaaactgtc	1020
tataccgtac cttatgccgc tgtcccatc ctgcaacgag aaggtcatth aaaatattct	1080
actacggtg gccaatatcg aagcaatagc tataaccaga aaagtcctta tgtatthcag	1140
ggggaattaa tttgggthtt accctgggat attacggctt atgggtggggc acaattctct	1200
gaggattacc gggcgthggc gctcggcctt ggctgaatc tgggtgtatt tgggtgcaaca	1260
tcttttgatg ttactcaggc taacagthcg cttgtggatg ggagcaaaca tcaagggcaa	1320
ttttatcgtt ttctttatth caaatcgtha gthcagacag gaacagcatt ccatattatt	1380
ggctatcgtt attcaaccca gggctthttac actthtaagt atacgacata ccaacaaatg	1440
tcagggactg ttgttgatcc aaaaacgtha gatgataaag attacgthta taaactggaat	1500
gattthttata acttgcgtha tagcaaacgt ggaaaatthc aggctagtgt atcgcaacct	1560
ttcggtaaact acgggtctat gtatthtatc gctagtcagc aaacatactg gaatactgat	1620
aaaaaagatt ctttatacca agthggthtat aacaccagta ctaagggtat ctatctaaat	1680
gttgcgtgga attacagtha atcaccaggg acaaatgcgg ataaaattgt ctcgctaaat	1740
gtctcattac ctataagtha ttggthtatct tccacgaatg atgggcgctc atcatcgaat	1800
gccatgactg caacgtatgg ttatagtcag gataaccacg gacaggtaaa ccaatatacg	1860
ggggtatctg gthctctgth ggagcagcat aatctcagth ataacataca acatggthtt	1920
gctaatacagg ataatagcag tagtggtthct gthggtgtha attatcgtgg ggcataatgg	1980
tccttgaatt ccgctacag ttacgataat gaaggthaatc acaaaataaa ctatggcatc	2040
agtggtgctc ttgttgthaca tgaaaatggt cttacgthga gtcaaccatt aggtgaaact	2100

aatgttttga taaaagcgcc tggagcgaat aatgtggatg ttcagcgggg gacaggaata 2160
 tccactgact ggcggtggata tgcagttggt ccttatgcaa cagaatatag acgtaataat 2220
 atttcattag atcctatgtc aatgaatâtg catactgaac tggatatcac ttcactgaa 2280
 gttattccgg gaaaagggtgc gttagtctgt gcagagtttg ctgctcatat cggatttcgt 2340
 ggtttgttca cagttcgtta tcgtaataaa tcagtcccat tcggtgctac agccagcgct 2400
 cagattaaaa acagtagtca aattaccggg attgtcggcg ataatggaca actttatctc 2460
 tcaggattgc ctttagaagg tgttattaat atccagtggg gagacggtgt tcagcaaaaa 2520
 tgtcaggcta attacaagct ccctgaaaca gaactggata atcctgttag ctatgcaact 2580
 ctggagtgcc gc 2592

<210> 85

<211> 507

<212> DNA

<213> Escherichia coli

<400> 85

atgggagcga tttatgttaa acgtttgatt ctgtcggtag cactgataat accgatagca 60
 tccaatgctt ctgatgcttt gaaccagccg agcagtagtc taaatgatgg tgttgagact 120
 ttttttattt cctgctttga tatgcctcag gaaacaacta ctgatatgga cgcttgctcag 180
 agagttcagt tagctcaggt tagttgggtt aagaataagt attcgggtggc cgccctgaat 240
 cgtttgaaac aagacaacaa ggatgatcca cagcgtctgc aggaattaac tgcttctttt 300
 aacgcggaaa gtgaagcttg gacagaatta attgagaaag cgtcaaagtc cgtccagggt 360
 gattatgtag gaggaactat agctggcact gcagttgcat cacgtcaaat tggttctctg 420
 gaattacaat cccacgatat ctgggagcac tggctacgat ctcgaggact caactcctcc 480
 tcttttgcca gaaccaaagt tcaaatc 507

<210> 86

<211> 2139

<212> DNA

<213> Escherichia coli

<400> 86

atggctatgt tcacaccttc attctcagga ctcaaaggtc gggcgctott ttcactgctt 60
 tttgcggcac cgatgattca tgcaacagac tctgtaacga ccaaagatgg cgaaacaatc 120
 actgttacag cagatgcaaa taccgcaact gaggcaaccg atggttatca acctctgagc 180
 acctccacgg cgacattaac cgatatgccg atgctggata tcccgcagggt ggtcaatacg 240

gtagcgatc aggttctgga aaaccagaat gcgacaacgc tggatgaggc gctttataac	300
gtcagtaacg tggtagacac caatacatta ggccgggactc aggatgcttt tgtacgccgt	360
gggtttggcg caaacccgga tggctccatc atgaccaacg gtctgcgaac cgtacttcct	420
cgtagtttca acgccgcaac agagcgtgtg gaagtgctaa aaggcccggc ctccacgctg	480
tatggcattc tcgatcctgg cggactgatt aacgtcgtga ccaagcgccc ggaaaaaaca	540
ttccatgggt cggtttcagc cacctcctcc agttttgggtg gcggcactgg gcaacttgat	600
atcacaggtc ccattgaagg cactcagctg gcgtatcgcc ttaccgggga agtgcaggat	660
gaagattact ggcgaaactt cggtaaagag cgcagtacat ttattgcccc gtcactcacc	720
tggtttgggtg ataatgcaac agtaaccatg ctctattccc atcgggacta taaaactcca	780
ttcgatcgtg gaacgatttt cgaccttacg acgaaacagc ccgtaaacgt tgatcgaaaa	840
atacgttttg acgaaccgtt taatattaca gatggtcagt ccgatctggc gcaactcaac	900
gcagaatac atctcaatag ccagtggaca gcgcgctttg attacagcta cagccaggat	960
aaatacagcg ataatcaggc gcgtgttacc gcgtatgatg caacgacagg aacactgaca	1020
cggcgtgttg atgcaactca gggatctacc cagcgtatgc atgctactcg tgcggatctg	1080
caagggaatg ttgatattgc cggattctat aatgagattc tgggtgggggt gtcatatgaa	1140
tattatgatc ttctgcgtac agatatgatt cgctgtaaaa aagctaaaga tttcaatata	1200
tacaaccctg tttatggtaa taccagcaaa tgtacaacgg ttccggcgtc ggacagcgat	1260
cagacgatca aacaggagaa ctactcagct tatgcacagg acgcgctcta tctgaccgat	1320
aactggattg ccgtcgccgg gatccgctat cagtattaca cgcaatatgc gggtaaaggc	1380
cgtcctttta atgtcaatac tgacagccgc gatgaacaat ggacgcccac actgggggta	1440
gtctacaaac tgacgccatc ggtatcctta tttgccaatt attcgcaaac atttatgccg	1500
cagtcgtcaa ttgccagcta cattggcgat ctccaccag aatcatctaa tgcttacgaa	1560
gtcggggcaa aattcgagct attcgatggg atcaccgcag atattgcgct gtttgatata	1620
cataaacgta atgtgttgta taccgaaagt attggtgatg aaaccatcgc caaaacggca	1680
ggccgcgttc gttcaagagg ggtagaagtc gaccttgccg gagcattaac tgaaaacatt	1740
aatatcattg ccagctacgg ctataccgat gcaaagggtc tggaagatcc tgattatgca	1800
gggaaaccat tgccgaatgt tctcgtcat accggttcgc tattcctgac ctatgatatt	1860
cataacatgc caggcaataa cacactgacg tttggcggtg gcggacatgg tgtaagccgt	1920
cgttcggcaa ccaatggggc tgactattat ctgcctggct atttcggtgc cgatgccttc	1980

170

gccgcataca aaatgaaatt gcagtatccg gtcactctgc aattaaacgt caaaaacctg 2040
 tttgataaaa cgtattacac ctcttccatc gccacaaata atctgggcaa ccagattggc 2100
 gatccgcgtg aagtgcatt cacggtgaaa atggaattt 2139

<210> 87

<211> 1818

<212> DNA

<213> Escherichia coli

<400> 87

atgaaaatat cgtggaatta tatatttaag aacaaatggc gatttcacat tacaagcatt 60
 tcactttttc ttatcatgct cgcggtttca atcgcttttt tgcacttgcg ttttaatacc 120
 ttgtccagta ccgataaaat gcggttgaa atgtataagt ccacattata ttccaccatc 180
 gagcaatttt atgttttacc ctatatgctc tcaacagacc atatcatccg tcaggcggtg 240
 attacgcctg acgatatgac gtccagcgaa ctcaatcaac gaattgcaca tttcaatact 300
 caactcaaaa ccgcagcaat atttattctg gatacccaag gtaaggccat cgcttctagc 360
 aactggcagg accccggcag ctatgtaggg caaaattata gctatcgccc ctattataaa 420
 cacgccatgt ctggcttaaa tggacgcttt tacggtattg gtagcactac gaatacaccg 480
 ggattcttcc tctctacaag tataaaagat aaaggaaaaa ttgtcggtgt tgtagtagta 540
 aaaataagtc ttaatgaaat tgaaaaagca tgggccgaag gtccctgaaaa tattatcgtg 600
 aatgatgaac atgggattat atttttaagt tcaaaatcgc catggcgaat gcgaacactg 660
 caacogttac ctgttcaggc aaaacaaaaa ctacaatcta cccgccaata tagtctcgac 720
 aatcttttac cggcggatta ttatccctgt tataccgtga gcaattttac tttcctgaaa 780
 gataaaaaag aacaactctg tttattcccg caatattata cgcaacaaat agccattcca 840
 gaatttaact ggaaaatgac aattatggtc cccttagata acctgtactg gtcattgggt 900
 atttcggttag tcattacact aattatttac ctgctgtttt tgttatttat taaatactgg 960
 agaatgcgat ctcatgcaca acaattatta acacttgca atgaaacatt agaaaaacag 1020
 gttaaagagc gtacatctgc cctggaattg atcaatcaaa aattaatata ggagataaaa 1080
 gagcgcagtc aagctgaaca agtattacaa attacgcgta gtgaactggc agagtccagc 1140
 aaactggcgg cgcttggaac gatggcaacc gaaattgccc atgaacaaaa tcaaccgtta 1200
 gccgccattc acgcacttac tgataacgcg cgtactatgc taaaaaaga gatgtatccg 1260
 caggttgaac agaacttgaa acatattatt tcagtgattg agcggatgac gcagctcatt 1320

171

tccgaactta aagcatttgc ctgcgcgccat cgcgtaccta aaggttctgc cgatgtcatc 1380
 aaagtgatgt atagcgccgt ggcggttactt aatcacagca tggagaaaaa taacattgag 1440
 cgacgaataa aagccccatc catgccgtta tttgtcaatt gcgatgagct cgggtcttgaa 1500
 cagatattca gtaatttaaat tagcaacgcc ttagattcta tggagggtag ctcttacaaa 1560
 cgactggata tcgccattcg ccaggcacaat aacaaagtta ttattaccat taaagacagc 1620
 ggtggcggtt ttgcacctga agttgtcgat cgcatttttg aaccattttt taccactaaa 1680
 cgtagaggaa tgggggttggg actggcaata gtcagcgaaa ttgtccgaaa ttcgaacggc 1740
 gcactccacg ccagtaatca tcctgaaggc ggcgcagtaa tgacattaac ctggcctgaa 1800
 tggggagaag aacatgaa 1818

<210> 88

<211> 303

<212> DNA

<213> Escherichia coli

<400> 88

gtgcttacac cacaacattt acgttgtgtg ttaacatgta gcgatttact gactcttttg 60
 agtgggtaccg ttatgtctca aatgcccctc tattttctta ataccacaaa gaaactcact 120
 gctcactatg aatggcttca aatcaacctg actgatacct acgaactagt taaaagggtta 180
 atgccgattc cttcactgga cgtgggtggt aaagtaggga aacttgtcct cccggagaaa 240
 gggcatcatg gtttttacct tgaagctgga gttgtctata gaacagtagc tccagaaaat 300
 cca 303

<210> 89

<211> 789

<212> DNA

<213> Escherichia coli

<400> 89

atgatgaaaa atacaggcta tatcttagct ctttgtctga cagcatcggg gcatgtccta 60
 gccatgatg tctggattac aggtaaacag gcagagaaca acgttaccgc agagattggt 120
 tatggtcata atttcccctc aaaggggaca attcctgaca gaagggattt ctttgaaaat 180
 cccgggcttt ataacgggaa agagacaata aactgaagc cagcgtccac ggattatgtc 240
 tataaaactg agtctgcaag caaagataat ggttacgttc tgtcaacgta tatgaaaccg 300
 ggatactggt cgagaacctc gtcaggatgg aaaccgggtca gccgggaggg cagaaatgat 360
 gtggcttact gtgaatttgt cactaaatat gcaaaatctt ttattcctgg tgaacagcag 420
 atgccagcac aactctatca gtctccaaca gggcatgagc ttgaaatcat tccgttatcc 480

gatataagtc gtttcagtga aaatgtgaag ctgaaagttc tgtataaaac gtccccgctc 540
gccggagcta tcatggagct tgactcggtc agttatctga catcatcccg tcatactcat 600
gcagttgagc acaaacatcc tgttcataaa gcagaactca cttttgtaac taatgaggat 660
ggtatcgtca cagtaccttc tcttcataac ggacagtggc tggcgaaagt ccaaaataag 720
aaaagttttc aggacaaaag cctgtgtgat gaaactgtcg atgtggcaac ctttaagcttc 780
tcccgaat 789

<210> 90

<211> 1134

<212> DNA

<213> Escherichia coli

<400> 90

atgggaaaaa taaaatattg gctaatagta ggatttatta tactttttgc gattttttac 60
attgctatta gtgacagga ttctacgctt tctaggttga aatcagcagg tgaaaacgga 120
gatgtagaag ctgagtatgc tttggggctc atgtatttgt atggagaaat tctggatggt 180
gattatcagc aggcaaagat ttggtatgaa aaagccgctg accaaaatga tccgcgtgcg 240
caggccaaac tcggtgtgat gtatgcaaat ggtctcgggg taaatcagga ttatcagcaa 300
tcaaaattat ggtatgaaaa ggcggtgctg caaaatgatg ttgatgcgca atttttgctt 360
ggggagatgt atgacgatgg tctcggggta agccaagact accagcatgc aaagatgtgg 420
tatgaaaaag cggctgctca aaatgatgag cgtgctcagg tcaatctcgc tgttctatac 480
gcaaagggtta atgggtgttga acaggattat cgacaggcca aaagctggta tgaaaaggct 540
gcagctcaaa atagtctga tgcgagttc gctcttgaa ttctgtatgc caatgctaata 600
ggtgtagagc aggactatca gcaggcaaaa gactggtatg agaaagcagc agaacaaaat 660
ttcgccaatg ctgagtttaa tcttggtatg ctctattaca aaggtgaggg tgttaaacia 720
aactttcggc aagccagaga atggtttgaa aaagccgcat ctcaaatca gccgaatgcc 780
caatataatt taggtcagat ttattactac ggtcaggggtg tgactcagag ctatcgacag 840
gcgaaagact ggtttgaaaa agcggcagag aaaggtcatg tcgatgctca atataatctc 900
ggtgtaatat acgaaaatgg tgaagggtgtg agtcagaact atcaacaggc aaaggcttgg 960
tatgaaaagg cagcctcaca aaatgatgag caggcgcagt tcgaacttgg cgttatgaat 1020
gaactgggtc aggggtgaaag catagacctg aaacaagcaa gacattacta tgagcgggtca 1080
tgtaataatg ggcttaagaa aggttgtgaa cgggttaaaag agttattata caaa 1134

<210> 91
 <211> 1962
 <212> DNA
 <213> Escherichia coli
 <400> 91
 atgaatgtaa tcagaactgt catttgtaca ttaattatac ttccggtggg attacaggca 60
 gcgaccagtc attcttctat ggttaaagat acaatcacca ttgtcgcgac aggaaatcag 120
 aacacggtat ttgaaacgcc gtcgatggtc agtgtcgtca cgaatgacac accgtggagt 180
 cagaatgcgg ttacatcggc cggcatgctg aaaggtgttg ccggtctcag ccagactggt 240
 gcaggacgga ccaatgggca gacctttaat ttacgcggt atgacaaaag cggggtactt 300
 gttcttggtg acggcggttcg ccaactcagt gacatggcaa aaagcagtgg cacttatctg 360
 gatccggcac tcgtcaaacg tatcgaagtt gtccgcgggc caaactccag tctgtacggc 420
 agtggcgggc tgggaggtgt agtggacttc agaactgccg atgcagcaga ttttcttccc 480
 cccggagaga caaacggttt aagtctgtgg ggaaatatcg ccagtgggtga ccacagcaca 540
 ggctcggggc tcacctggtt tggtaaaact ggaaaaacag atgcgctcct ttctgtcatt 600
 atgcgtaaaa gaggtaatat ctatcaaagt gatggtgagc acgcacctaa caaggaaaaa 660
 cctgcagccc tgtttgcgaa aggtctgtgc ggtataacag acagtaacaa agcaggtgcc 720
 agcttgcgtc tctaccggaa taacaccact gaaccgggca attccactca gacacatggt 780
 gacagcggcc tgcgtgacag aaaaacagta caaatgacg tacagttctg gtaccagtac 840
 gctcctgtgg ataacagcct catcaatgta aagtcaacgt tatactctcag tgatatcact 900
 atcaagacaa acggtcacaa caaacgggca gaatggagaa acaacagaac ctccggtggt 960
 aatgttggtca acaggagtca tactctgatt tttccgggag cccatcagtt aagttatggc 1020
 gctgaatatt accgtcagca gcagaagcca gaaggctctg ccacactata tccggaagga 1080
 aacattgact ttacatcggt gtatttccag gatgaaatga caatgaaaag ctaccgggtt 1140
 aacattatcg tcggttcccc ctatgaccgg tacaagagct tcaatccccg tgccggagaa 1200
 ctgaaagccg aacgcctgtc cccaagggcg gcgatttcag tctaccgac agactggctg 1260
 atgatgtacg gctccatatc ctctgcattc cgagcgccca caatggcaga aatgtacagg 1320
 gatgatgtac atttttaccg caagggtaaa cccaattact gggttcctaa ccttaatctg 1380
 aaaccagaaa ataacatcac ccgtgagatt ggcgcaggta ttcaactgga tggcctgctt 1440
 acagacaatg accggctgca gttaaaaggc ggatatttcg gaacggatgc cagaaactat 1500
 attgccacac gcgtggatat gaaacggatg cgttcttatt cttataatgt atcccgggcc 1560

174

cgtatctggg gatgggatat gcagggtaat taccagtctg attatggtga ctggatgctt 1620
 tottataaacc ggacggaaag tatggatgcc agcagcaggg aatggctggg ctccggcaat 1680
 cctgacacac ttatcagtga catcagcata cctgttggtc atagaggcgt ttatgccgga 1740
 tggcgtgctg aactttcagc atcagccacg catgtgaaaa aaggcgatcc ccatcaggct 1800
 ggttatacca tacattcctt ttcactgtct tataagcctg taagtgttaa aggctttgag 1860
 gcgtcagtaa ctctggataa tgccttcaac aagcttgcca tgaatggcaa aggtgtgccg 1920
 ctttcaggca gaactgtcag tctttataacc cgttatcagt gg 1962

<210> 92

<211> 4128

<212> DNA

<213> Escherichia coli

<400> 92

atgaataaaa tatacgtctt aaaatatgtt tatattacta acacagtaaa gggtgtctct 60
 gaactagccc gaagggtatg taaaggaggt accgcagag gaaaaagact ttcagtactt 120
 acctctctgg cactatctgc attactccca accgttgctg gtgcatcaac gggtgggtggc 180
 aacaatcctt accagacata ccgcgacttt gcagaaaaca aagggcagtt tcagggtggc 240
 gcaacaaaca ttctatcttt taataataaa ggggaattag taggacatct tgataaagcg 300
 cccatgggtg attttagcag tgtgaatgta agctcaaata ccggcggttg aacattaatt 360
 aaccgcgaat atatagccag tgtaaaacat aataaaggat atcagagcgt cagcttcggt 420
 gatggtcaga acagttacca tattgtggat cgtaatgaac acagttcatc tgatctccac 480
 acaccaagac ttgataagct cgtaactgag gttgctccgg ctaccgtaac cagctcatca 540
 acagctgata tattgaaccc ttcaaaatac tcggcattct acagggtggg ttcgggaagt 600
 cagtatattc aggatagtca gggtaagcga cattgggtaa cagggtgggtg tggttatctg 660
 acaggaggaa tactcccgac atcattcttt tatcacggct cagacggcat tcagctgtat 720
 atgggggggca acatacatga tcatagcatc ctgccctctt ttggagaggc cggcgacagt 780
 gggtctccat tatttggtct gaatacggcc aaagggcagt gggaaactggc cgggtgtttac 840
 tcgggagtag gaggggggac caatttgata tattctctta ttctcagag tttctctca 900
 cagatctatt cagaggataa tgacgctccc gtctttttta atgcctcatc cggcgccccc 960
 ctgcaatgga aatttgacag cagcaccggc actggctctc tgaaacaggg ttccgatgaa 1020
 tatgccatgc acggggcaaaa aggttctgac ctgaacgcag gtaaaaatct gacattcctg 1080

ggacataatg gtcagattga cctggaaaac tctgtcacgc aggggtgcggg ttcactgaca	1140
tttactgatg actacactgt caccacttca aacggaagta cctggaccgg ggccggtatt	1200
attgtggaca aggatgcctc cgtaaactgg cagggttaatg gtgtgaaagg tgacaacctg	1260
cataaaatcg gcgaaggaaac cctggttgta cagggaaaccg gtgttaatga gggcggcctg	1320
aaagtcgggg atgggaccgt tgtcctcaat cagcaggctg acagttcagg acacgttcag	1380
gcattcagta gcgtgaatat tgccagcggc cgcccgacag tcgtgctggc agacaaccag	1440
cagggttaatc cggacaatat atcctggggc taccgggggg gggttctgga tgttaacggg	1500
aatgacctga catttcataa gctgaatgcc gccgattatg gcgcaactct cggtaacagc	1560
agtgataaaa cggctaatat cactctggat tatcagacgc gtccggcaga cgtaaaagtt	1620
aatgaatggt catcatcaaa caggggaaca gtaggttcat tataatattta taataatccc	1680
tataactcata ccgtcgatta ttttatcctg aaaacaagta gttatggctg gttccctacc	1740
ggtcaggta gtaacgagca ctgggaatat gtcggacatg accagaacag tgcacaggca	1800
ctgcttgcaa acagaattaa taataaaggg tatctgtatc atggcaagtt gctgggaaat	1860
attaatttct caaataaagc aaccccggtt acaaccggcg catttggttat ggacggctca	1920
gcgaatatgt ccggtacatt tactcaggaa aacggctcgtc tgaccattca gggccaccgc	1980
gttatccatg cttcaacgtc tcagagtatt gcaaatacag tctcgtctct gggcgacaat	2040
tccgttctga cacagcccac ctcatTTTaca caggatgact gggagaacag gacgttcagc	2100
tttgggtcgc tcgtgttaaa agatacagac tttgggtctgg gccgcaatgc cacactgaac	2160
acaaccatcc aggcagataa ctccagcgtc acgctgggcg acagtcgggt atttatcgac	2220
aaaaaagatg gccagggaac agcatttacc cttgaagaag gcacatctgt tgcaactaaa	2280
gatgcagata aaagcgtctt caacggcacc gtcaacctgg ataatcagtc agtgctgaat	2340
atcaatgaga tattcaatgg cggaatacag gogaacaaca gtaccgtgaa tatctcctca	2400
gacagtgccg ttctggagaa ctcaacgctg accagtaccg ccctgaatct gaacaaggga	2460
gcaaatgttc tggccagtca gagttttggt tctgaocggtc cgggtgaatat ttctgatgcc	2520
accctgagtc tgaacagccg tcttgatgag gtatctcaca cacttttacc tgtatacgat	2580
tatgccgggt catggaacct gaaggagac gatgcccgc tgaacgtggg gccgtacagt	2640
atgttgctcag gtaatatcaa tgttcaggat aaagggactg tcaccctcgg aggggaaggg	2700
gaactgagtc ctgacctgac tcttcagaat cagatgttgt acagcctgtt taacgggtac	2760
cgcaatacct ggagcgggag cctgaatgca ccggatgcc cgcgcagcat gacagacacc	2820

cagtgggtcga tgaacggaaa ctccacggca ggaaatatga aacttaaccg gacaatagtc 2880
 ggttttaacg ggggaacatc atcgttcacg aactgacaa cagataatct ggacgcgggt 2940
 cagtcagcat ttgtcatgcy tacagacctt aacaaggcag acaaactggg gataaacaag 3000
 tcggcaacag gtcatgacaa cagcatctgg gttaacttcc tgaaaaaacc ctctgacaag 3060
 gacacgcttg atattccact ggtcagcgca cctgaagcga cagctgataa tctgttcagg 3120
 gcatcaacac ggggtgtggg attcagtgat gtcacccccca cccttagtgt cagaaaagag 3180
 gacgggaaaa aagagtgggt cctcgatggg taccagggtg cacgtaacga cggccagggt 3240
 aaggctgccg ccacattcat gcacatcagc tataacaact tcatcactga agttaacaac 3300
 ctgaacaaac gcatggggca tttgagggat attaacggcg aagccggtag gtgggtgcgt 3360
 ctgctgaacg gttccggctc tgctgatggc ggtttcactg accactatac cctgctgcag 3420
 atgggggctg accgtaagca cgaactggga agtatggacc tgtttaccgg cgtgatggcc 3480
 acctacactg acacagatgc gtcagcaggc ctgtacagcg gtaaaacaaa atcatggggg 3540
 ggtggtttct atgccagtg tctgttccgg tccggcgctt actttgattt gattgcaaaa 3600
 tatattcaca atgaaaacaa atatgacctg aactttgccg gagctggtaa acagaacttc 3660
 cgcagccatt cactgtatgc aggtgcagaa gtcggatacc gttatcatct gacagatacg 3720
 acgtttgttg aacctcaggc ggaactgggc tggggaagac tgcagggccca aacatttaac 3780
 tggaacgaca gtggaatgga tgtctcaatg cgtcgtaaca gcgttaatcc tctggtaggc 3840
 agaaccggcg ttgtttccgg taaaaccttc agtggttaagg actggagtct gacagcccgt 3900
 gccggcctgc attatgagtt cgatctgacg gacagtgtcg acgttcacct gaaggatgca 3960
 gcggggagaac atcagattaa tggcagaaaa gacggtcgta tgctttacgg tgtgggggta 4020
 aatgcccggg ttggcgacaa tacgcgtctg gggctggaag ttgaacgctc tgcattcggt 4080
 aaatacaaca cagatgatgc gataaacgct aatattcggt attcattc 4128

<210> 93

<211> 1047

<212> DNA

<213> Escherichia coli

<400> 93

atgattacac tttttcgact actggcgatt ctttgccctt tttttaacgt ttcagctttt 60
 gctgttgatt gctatcagga tgggtacaga ggaacaaccc tcataaatgg agatttacca 120
 acgttcaaaa ttccagagaa tgcgcaacct gggcaaaaaa tttgggagag cggagatatt 180

aatatcacag tttattgtga caatgcacca ggatgggtcaa gtaataaccc atcagaaaat	240
gtctatgcct ggatcaaatt gccccaaata aatagtgccg atatgttgaa taatccgtat	300
ttaacatttg gcgtgactta taatgggtgta gattatgaag ggacaaatga aaaaattgat	360
actcatgcgt gcctggataa atatgaacaa tactataatg ggtattatca tgaccctgta	420
tgcaatggca gcactcttca aaaaaatgta acattttaacg cccattttcg cgtctatgta	480
aaattcaaaa gccgcccggc aggagatcag acggtaaact ttggcacagt caacgtgctg	540
caattcgacg gtgaaggcgg ggcgaaacatg gcccccaacg cgaaaaattt acgctatgcg	600
attacggggg tagataatat ttcattcctt gactgtagtg tcgacgtccg ctttccccg	660
gaaagtcaga tagtcaattt tgggcagatc gctgcgaatt ccattgcaac tttcccaccg	720
aaggcagcat tcagcgtttc taccataaaa gacattgcgt ctgattgtac cgaacagttt	780
gatgttgcaa ccagtttctt tacttcagat acattatatg acaatacgca tctggaaata	840
ggtaacggct tgctcatgcg aattactgat caaaaaacgc aagaagatat taaatttaac	900
cagttcaa at ttttagtac ttatattccc ggtcagagtg cggcaatggc aaccgcgat	960
taccaggccg aattaacca aaaacctggg gaaccactcg tctatggccc atttcagaaa	1020
gacctgatag ttaaaatcaa ctaccac	1047

<210> 94

<211> 2520

<212> DNA

<213> Escherichia coli

<400> 94

atgaacaata aaaacacggt ttcccgggat aagttatccc atgcaattaa aaatgccctg	60
tctggcggtg tgtgttcctt actcttcggt ttgccagtcc acgccgtaga attcaacgtc	120
gatatgattg acgcagaaga ccgtgagaat atcgacatct ctcgttttga gaaaaaaggc	180
tatatcccc ctggtagata cctcgttcgt gtgcaaataa ataaaaatat gttgccacaa	240
acgttaatac tggaatgggt aaaagccgat aatgaaagtg gttcgttact ctgcttaacc	300
aaagaaaatt tgactaattt cgggtcttaac acggaattta ttgaatcatt gcaaaacata	360
gctggcagcg aatgtctcga tttaagccaa cgtcaggagt taacgacacg acttgataaa	420
gctacgatga tattatcgct aagtgttccc caggcatggg taaaatacca ggcaacaaac	480
tggacgccac cagagttttg ggataccggg atcacccggg ttatccttga ttacaacgtg	540
tacgccagcc agtatgcccc acatcacgga gacagcacc aaacgcgcag ctccctatgg	600
acgttaggct ttaacctcgg cgcattggcg ttacgtagcg attaccaata taatcagaat	660

tttgctgatg gacgctcggg aaaccgcgac agcgaatttg cgcgaactta tctgtttcgc	720
cctatcccct cctggctcgc aaaattcact atggggccagt acgacctgag ctccaatctt	780
tacgatacct tccactttac tggcgcatcg ctggaaagtg atgaaagcat gctgccgccca	840
gatttacagg gttatgcgcc acaaattacc ggcacgcgc agaccaacgc gaaagtaact	900
gtggcacaaa atggctcgtg actttatcaa accactgtcg cgccaggccc ttttactatt	960
tctgatttgg ggcaatcgtt tcaggggag ctggatgtca cagtggaaga agaagatggc	1020
cgcaccagca ccttcagggt tggctccgca tccattccct atttaaccg taaagggcaa	1080
gtgcgctata aaacgtcact gggaaaaccg acatccgtcg ggcataacga tatcaataat	1140
ccctttttct ggacggcgga agcctcctgg ggctggctga acaatgtgtc gttgtatggg	1200
gggtggcatgt tcaccgctga tgattatcag gctatcacta ccggtattgg ctttaacctt	1260
aaccaattcg gttcgtttc ttttgatgtc actggagcag acgcgtcttt acagcaacaa	1320
aatagcggca atctgcgtgg ttacagctat cgcttcaact atgcaaagca tttcgaatcg	1380
acaggcagtc agattacctt cgcgggttat cgcttctcag ataaagatta cgtgtcgatg	1440
agtgagtacc tcagctcgcg taatggcgat gagtcaatcg ataataaaaa agagagttat	1500
gtcatttcct tgaaccagta ctttgaaacg ctggaattaa actcttatct caacgttaca	1560
cgcaatactt attgggacag cgccagcaat accaactact ccgtatctgt aagcaaaaac	1620
tttgatattg gcgatttcaa aggtatatct gcacgctgg cagtaagtcg aatccgctgg	1680
gatgacgacg aagagaatca atattacttc tctttctctc tacctttaca acaaaaccgc	1740
aacatctcct acagtatgca gcgaacggga agcagtaata cttcgcagat gatttcctgg	1800
tacgattcat cagatcgcaa caatatctgg aatatttcag cgtcggcaac ggacgacaat	1860
atacgtgatg gcgaaccaac actgcgcggc agctaccagc actattcgcc gtggggacgc	1920
ctgaacatta atggcagtg acagccgaat cagtacaatt ctgttaccgc aggctgggtac	1980
ggttcactta ccgctacag tcattggtgt gcccttcacg attatagcta tggcgataac	2040
gcccgcata tggtcgatac cgatggcatc tccggcattg aaatcaactc taaccgtacc	2100
gttaccaacg ggctgggcat cgccgtgata ccttcgttat cgaactacac cacctccatg	2160
ttgcgggtga acaataacga tctgccagaa ggtgtcgatg tcgaaaactc ggttattcgt	2220
actacgctca cccagggtgc catcggtac gcaaaactga atgccaccac cggataccaa	2280
atcgtcggcg ttattcgtca ggaaaatggc cgcttcctc cactaggtgt gaatgtcacg	2340

gataaagcga caggtaaaga tgtgggcctg gtagcggaag atggcttcgt ttatctcagc 2400
 ggtattcagg aaaacagtat tctgcattta acctgggggtg ataatacctg tgaagtcacg 2460
 ccgccaaacc aaagtaacat tagtgaaagc gcgataattt taccttgtaa aacagtcaaa 2520

<210> 95

<211> 507

<212> DNA

<213> Escherichia coli

<400> 95

ttgatgaaca caaaacagtc tgttgctcaa ctgcgcgtac cgcaccgcaa gcgcctttca 60
 tcaacgatgg tgggtggcgt gttactttgt gtggttgctg gcgcggtgat gattaatgcc 120
 gctgattttc cagcaactgc cattgaaacg gatcccggtg caagtgcctt ccctaccttc 180
 tatgcctgtg ccctgattgt gctcgtctgc ttgctgggtga tacgcgatct tttgcaggca 240
 aaaccagcct cttgcgcaa cgcacaggaa aaaccggcat tcaggaaaac agcaacagga 300
 attgcggcaa ccgcgtttta tattgtggcg atgagctact gcggttatct cattactact 360
 cctgtttttcc tcatcgtcat tatgacgttg atgggctaca ggcgatgggt actcacaccg 420
 ggtattgcgc tgctgttaac ggcaatcctc tggttgctgt ttgtcgaagc gttacagggtg 480
 ccattgcctg tcggcacatt tttcgaa 507

<210> 96

<211> 933

<212> DNA

<213> Escherichia coli

<400> 96

atggtacttc ttgcaggcgc tgccctcagc attgcgcctg tacaggcagc ctccctaccca 60
 accaaacaga tcgagttagt cgttccttac gctgccggag gcggtacgga tctggttgcc 120
 cgtgcctttg ctgatgccgc caaaaaccat ttaccgctca gcacgggggt tatcaataaa 180
 cctggcggag gcggtgctat cggcctgagt gaaatcgccg ctgcccggcc taacggttac 240
 aaaattgggt taggcacggg tgaactgacc acccttccca gcctcggaat ggtgcgtttt 300
 aaaaccagcg actttaaac cattgcccgt ctgaatgagg atccggctgc tatcacagtc 360
 cgtgccgatg cgccgtggaa tagctatgaa gaatttatgg cttactccaa agcgaatccc 420
 ggaaaagtac gcattggtaa ctcaggcacc ggagctatct ggcactctggc ggcagctgca 480
 ctggaagaca aaacgggcac aaagtgttct catgtcccgt atgacggcgc agcccctgcc 540
 attacaggcc tgtagggcgg gcatattgaa gcggtttccg taagcccagg agaagttatc 600
 aaccatgtga atggcggcaa gctgaagaca ctggtagtga tggcggatga gcgaatgaaa 660

180

accatgcctg acgtcccgac gttaaaagag aaaggcggtg atctctccat cggcacctgg 720
 cgcggcctga ttgtgtcgca aaaaacgccg caggatgtgg tggatgttct ggcaaaggca 780
 gcaaaagaga cggtgaaga gcctgcattc caggatgcac tgcaaaagtt gaatctcaac 840
 tatgcatggc ttgacgctgc cagcttccag acccaaata gcaaacagga aaagtacttt 900
 gacgagttgc tgactcgcct gggcctgaaa aaa 933

<210> 97

<211> 2166

<212> DNA

<213> Escherichia coli

<400> 97

atgctgcgat ggaaacgctg tattattcta acatttatct ctggtgctgc tttcgcggcg 60
 ccagagataa atgttaagca aaacgaatcg ttacctgatt taggtagcca ggcagcacia 120
 caggatgaac aaaccaacaa gggtaaactc ctgaaagagc gggagagcca ttacgtcatc 180
 aactccgcca cgcaagggtt tgaaaacttg acccctgagg cgctggaatc tcaggccaga 240
 agctatctgc aaagtcaaat cacctcaacc gcacaatctt atattgaaga cacactctct 300
 ccctacggta aggtccgttt gaacctctcc attggtcagg gggcgatct ggatggcagt 360
 tccatcgatt attttgttcc ctggtacgat aatcaaacca ctgtttatct cagccaattt 420
 tctgcgcaac gaaaagaaga tcgtacgac gggaaatattg gccttggggg aaggtataat 480
 tttgataaat atctattggg tggaatatata ttttatgatt atgactttac cgtggacat 540
 cgccgttttag gtttaggcgc cgaagcctgg acggattatt taaaattctc aggcaactat 600
 tatcaccac tttctgactg gaaagactct gaagatttcg acttttatga agaacgcct 660
 gcgcgcgggtt gggatattcg tgccgaagtc tggttacctt cttatccga actggggggc 720
 aaaattgtct tcgagcaata ttacggcgat gaagtcgcc tttttgtac ggataatttg 780
 gagaaagatc cctacgcgtt aacgcttga btgaattatc aaccagtgc gttactgaca 840
 gttgggacgg actataaagc ggggaccgga gataacagt atgtcagcat taatgccact 900
 cttaattatc agttcggcgt tccgctaaaa gatcaattgg atagcgataa agtgaaagcg 960
 gcgcactcgc tgatgggcag ccgtcttgat ttcgttgagc gtaataactt tattgttctg 1020
 gaatacaaag aaaaagatcc gcttgatgtc accctgtggg tgaaagcgga tgccaccaac 1080
 gagcaccctg agtgcgtcat taaggacact cccgaagcgg ccgtcggctt ggaaaaatgt 1140
 aagtggacca ttaacgcact cattaatcat cattacaaaa tcgttgccgc ctctggcgag 1200

181

gcgaaaaaca atgccgcccc caccgtggtg atgccgggta tcaaagagaa tactctgaca 1260
 gagggtaaca ataaccactg gaacctggtg ctgcctgcct ggcagtacag ttccgatcaa 1320
 gccgaacaag aaaaactcaa tacctggcga gtacgtctgg cgctggaaga tgaaaagggc 1380
 aaccgacaga actctggcgt ggtggaaatc accgttcagc aggaccgtaa aatagagttg 1440
 attgttaata acatcgcgaa cccagaagag aacaaccaca gccacgaagc cagcgcacag 1500
 gcagatggcg ttgatggtgt agtgatggat ctcgatgtaa ccgacagctt tggcgataac 1560
 accgaccgca acggcgatgc gttgccggaa gataacctta cgcctcagct ttacgacgcg 1620
 caggacaaac gagtgcggtt aaccaacaag ccctgctcga ccgataaccc ctgcgttttt 1680
 attgccaac aagataaaga aaagggcact gtcacctct ccagtacctt acctggcacc 1740
 tatcgctgga aagcaaaagc cgcgccctac gatgacagta actatgtgga tgtcactttc 1800
 ctgggggcag aaattggtgg gctaaatgct tttatctatc gtgtgggggc ggctaaaccc 1860
 agcaacctga taggtaaaga taaagaaccg ttgccgtcaa caacatttat cgatttggtt 1920
 tatggcgcgca caacaataaa gacgggtgtct tccagcaggt cgaaaaacct gacgaagaga 1980
 tgggtgcagta cgactacaag tgggaattta ccggcaagag catcaatggt aagtgggtgc 2040
 acaggcgaac actccaatga ggacattgtg attccggcca ctaaccgtga agcggcgcaa 2100
 acctatggcg cacaagcggg agatggcttg cagggatacg gtttacgcgt gctgtatacc 2160
 aaaaaa 2166

<210> 98

<211> 957

<212> DNA

<213> Escherichia coli

<400> 98

atgaagcagg ataaaagacg cggctctgacc cggatcgcat tagcgctggc actggcaggt 60
 tattgtgtgg cacctgtggc gctggctgaa gacagcgctt gggtcgacag cggtgaaacc 120
 aatattttcc aggggaccat tccgtggctc tattcggaag ggggaagtgc tacgacagat 180
 gccgaccgtg taacgttgac ttctgatcta aaaggcgctc gcccgcaagg catgaaacgg 240
 acaagcgttt ttactcgggt gataaatatt ggtgataccg aaggcgacgt ggatcttggt 300
 ggattgggcg ataacgcgaa aactatcgat actatccgct ggatgagcta caaggatgcg 360
 cagggggggg atccaaaaga gctggcaacg aaggtgacca gttacactct taccgatgcc 420
 gaccgtggtc gctatatcgg tattgaaatt acgccaacca cgcagaccgg tacgccaac 480
 gtcgggactg cgctgcatct ttatgacgtt tctactgccg gcggcgggcg aagcgacagc 540

gataacggtg caccggggcc ggtgggtaac cagaacctga aagtcgccat ctttggtgat 600
 ggtaccagta tcaaccttat caacggtagc acaccaatcg aacttggcaa aacctacgtg 660
 gccaaactgt actcggatga gaacaaaaat ggcaagtttg atgcgggtac cgatgctgac 720
 gtcaccgcca attatgactt ccgttgggta ctttctggca gcagccaaca gcttggcact 780
 tcgggtggca tcgttaactc aagcttcgat aataacaatt tggatcatcc tgcgaccaac 840
 gacgaagcca gaaccaacct taacggccct gcgcgcgatg gaaaagaggc actttccatc 900
 ccgaccaacg gcgacggggt acagggttac aaacttcaca ttatttatac acacaaa 957

<210> 99

<211> 1887

<212> DNA

<213> Escherichia coli

<400> 99

atgaagaaag tgctcactct ctactactg gctctgtgtg tgtctcatag tgcagtagca 60
 gcaaactata cggtcaataa cgataatatt gccctctcgt ttgatgatac aaactcgacg 120
 attgtgctga aggaccgtag aactaaccat ccgatcacac cacaggaatt gttctttctg 180
 acactaccgg atgagacaaa aatccacacc gcgatttca aaatcaagca catcaaaaaa 240
 caggacaatg cgattgtcat cgactttacg cgcccgagatt ttaacgtaac agtgcagttg 300
 aaccttgtga agggaaaata tgccagcatc gactacacta ttgccgccgt tgggcaacca 360
 cgagacgtcg ccaagattac cttcttcccg accaaaaaac agtttcaggc tccttacgta 420
 gacggcgcaa tctactagctc accgatcatt ggggactcgt tctttatcct gccgaataaa 480
 ccgatcgtga atacctacgc ctatgaagca acaaccaatc tcaacgtaga actgaaaact 540
 ccaattcagc cagagacgcc ggtagcttt accacctggg tcggtacttt cccggaaacc 600
 agccagttgc gacgcagtgt gaaccagttt attaatgccg tacgtccacg tccgtacaag 660
 ccttattttgc attacaacag ttggatggat atcggctttt tcaactcgtc caccgaacag 720
 gatgttctgg gacgcatgga cgaatggaac aaggaattca ttagcggccg cggagtggcg 780
 ttagacgctt ttctgctgga cgatggctgg gacgatctta ccggacgctg gttatttggc 840
 ccggcattca gcaacggttt tagcaaagta cgagagaaag ccgatagcct gcacagctcc 900
 gttgggctat ggctttcacc gtgggggggt tacaataagc cgcagcgacg ttcgcgtttc 960
 gcatgcaaaa gagtatgggt tcgaaaccgt ggacggcaag ctggcgcttt cgggagcgaa 1020
 ctacttaaaa acttcaatga gcgatcatt aatcttatca aaaatgaaca cattacctcg 1080

183

tttaaactcg acggaatggg gaacgccagt tcacatataa agggtagccc gttcgccctcg 1140
 gattttgatg cgtcaatagc tctgctgcac aatatgcgca gagcaaaccg gaatctatct 1200
 atcaacctga ccaccggcac caacgccagc ccgtcctggg tgttctatgc tgattctatc 1260
 tggcgctcagg gggatgatat aaacctgtat ggccccggca cgccggtgca gcagtggata 1320
 acatatcgtg atgccgagac ataccgctct attgtacgta aaggcccgtt attcccgtg 1380
 aactcgctga tgtaccacgg gatagtcagc gccgagaatg cctattacgg gttagagaag 1440
 gtgcaaacgg acagcgactt tgccgatcag gtctggagct acttcgagc cggcacccag 1500
 ctgcaggagc tgtatattac cccgtccatg ctgaacaagg tgaagtggga tacgctggcg 1560
 aaggctgcaa aatggctgaa ggaaaatgcc agcgtgctgg ttgataccca ctggattggc 1620
 ggcgacccaa cggcgcttgc cgtgtacggc tgggcctcct ggagcaaaga caaagccatt 1680
 ctcggtttgc gcaaccatc ggataagcca cagacctact atctggattt ggcgaggat 1740
 ttcgaaatac cggcaggaaa cgcggcgagc tttagtctga aagcgggata cggcagcaat 1800
 aaaacagtgc ccgttgagta taaaaacgcg acggtgatta cgttgagcc gctggaaacg 1860
 ctggtgtttg aggcggtgac cattaac 1887

<210> 100

<211> 5334

<212> DNA

<213> Escherichia coli

<400> 100

atgaacaaaa tatttaaagt tatctggaat ccggcaacag gcagttacac cgttgccagc 60
 gaaacggcga agagccgtgg taaaaaaagc gggcgagta agctgttaat ttctgcactg 120
 gttgcgggtg ggttgttgtc gtcgtttggg gcaagtgcag ataattacac tgggcagcca 180
 actgattatg gcgatggctc agcaggtgac ggctgggttg ctatcggtaa aggggcaaaa 240
 gcaaatacct ttatgaacac tagtggcgcg agtacagctt taggatatga cgcgatagcc 300
 gaaggtgagt acagttctgc catcggttca aaaacccttg caactggtgg agcatccatg 360
 gcgttcgggg ttagtgcaaa agcaatgggt gacagaagtg tcgcgctagg tgcacgtca 420
 gtagcaaatg gcgatcggtc gatggctttt ggtcgttacg caaagacgaa tgggtttaca 480
 tctcttgcta ttggggactc ctcccttgcc gatggtgaaa aaactattgc gttaggaaat 540
 acggctaaag cttacgaaat tatgagcatc gccctcggtg ataatgccaa tgcgtcaaaa 600
 gagtatgcaa tggcgctggg agcaagtagc aaagctggcg gtgctgatag cctcgcatc 660
 ggcagaaaat ctacagctaa tagcactggc tcaactggca taggtgctga cagtagcagt 720

togaacgata acgccatcgc gatagggaaac aaaacgcaag ccctgggagt gaattcgatg	780
gccctgggta atgcaagtca ggcattctggc gaatccagta ttgcattagg taacaccagt	840
gaagccagcg aacaaaatgc gattgcgctg gggcaaggta gcattgcaag caaagtgaac	900
tcaatcgcgt tgggaagtaa cagttttgtcc tcgggagaga atgccatcgc attgggagag	960
ggtagtgccg ctgggtggcag caacagcctt gctttcggta gccagtccag ggcaaacggc	1020
aatgattctg tcgccatcgg tgtaggggct gcagcagcga ccgacaattc tgtcgctatc	1080
ggcgaggat cgaccacaga tgcaagcaat acggtttcag ttggcaacag cgcaacaaaa	1140
cgcaaaattg ttaatatggc tgctgggtgcc ataagcaaca ccagtaccga tgccatcaac	1200
ggctcacagc tttatacgat cagtgattca gtcgccaagc gactcggagg aggcgctact	1260
gtaggcagcg atggcacctg aaccgcagta agctacgcgt tgagaagcgg aacctataat	1320
aacgtgggtg atgctctgtc aggaatcgac aataataccc tacaatggaa taaaaccgcg	1380
ggggcggttca gcgccaatca cggtgcaaat gccaccaaca aaatcactaa tgttgctaaa	1440
ggtacgggtt ctgcaaccag caccgatgta gtaaacggct ctcaattgta cgacctgcag	1500
caggatgtc tgttggtggaa cggcacagca ttcagtgcg cacacggcac cgaagccacc	1560
agcaaaatca ctaacgtcac cgctggcaac ctgactgcg gcagcactga cgccgttaac	1620
ggctctcagc tcaaaaccac caacgacaac gtgacgacca acaccaccaa catcgccact	1680
aacaccacca atatcaccaa cctgactgac gctgttaacg gtctcgggtga cgactccctg	1740
ctgtggaaca aagcagctgg cgcattcagc gccgcgcacg gcaccgaagc caccagcaaa	1800
atcaccaacg tcaccgctgg caacctgact gccggtagca ctgacgccgt taacggctcc	1860
cagctcaaaa ccaccaacga caacgtgacg accaacacca ccaacatcgc cactaacacc	1920
accaatatca ccaacctgac tgacgctgtt aacgggtctcg gtgacgactc cctgctgtgg	1980
aacaaaacag ctggcgctt cagcgccgcg racggcactg acgccaccag caagatcacc	2040
aacgtcaccg ctggcaacct gactgccggc agcactgacg ccgttaacgg ctcccagctc	2100
aaaaccacca acgacaacgt gacgaccaac accaccaaca tcgccactaa caccaccaat	2160
atcaccaacc tgactgacgc tgttaacggc ctcggtgacg actccctgct gtggaacaaa	2220
acagctggcg cattcagcgc cgcgcacggc actgacgcca ccagcaagat caccaatgtc	2280
aaagccggtg acctgacagc tggcagcact gacgcggtta acggctctca gctcaaaacc	2340
accaacgata acgtgtcgac caacaccacc aacatcacca acctgactga cgctgttaac	2400

ggtctcgggtg acgactccct gctgtggaac aaaacagctg gcgcattcag cgccgctcac	2460
ggcactgacg ccaccagcaa gatcaccaat gtcaaagccg gtgacctgac agctggcagc	2520
actgacgccg ttaacggctc ccagctcaaa accaccaacg ataacgtgtc gaccaacacc	2580
accaacatca ctaacctgac ggattccgtt ggcgacctta aggacgattc tctgctgtgg	2640
aacaaagcgg ctggcgcatc cagcgccgag cacgggtaccg aagctaccag caagatcacc	2700
aacttactgg ctggcaagat atcttctaac agcactgatg ccattaatgg ctcacaactt	2760
tatggcgtag cggattcatt tacgtcatat cttgggtggtg gtgctgatat cagcgatacg	2820
ggtgtattaa gtgggccaac ctacactatt ggtgggtactg actacactaa cgtcgggtgat	2880
gctctggcag ccattaacac atcatttagc acatcactcg gcgacgccct actttgggat	2940
gcaaccgcag gcaaattcag cgccaaacac ggcattaata atgctcccag tgtaatcact	3000
gatgttgcaa acggtgcagt ctcgctccacc agcagcgacg ccattaacgg ttcacaactt	3060
tatggtgtta gtgactacat tgccgatgct ctgggcggga atgctgtggt gaacactgac	3120
ggcagtatca ctacaccaac ttatgccatc gctggcggca gttacaacaa cgtcgggtgac	3180
gcgctggaag cgatcgatac cacgctggat gatgctctgc tgtgggatac aacagccaat	3240
ggcggtaacg gtgcatttag cgccgctcac gggaaagata aaactgccag tgtaatcact	3300
aacgtcgcta acggtgcagt ctctgccacc agcaacgatg ccattaatgg ctcacagctc	3360
tatagcacta ataagtacat cgctgatgag ctgggtggtg atgcagaagt caacgctgac	3420
ggtactatca ctgcaccgac ttacaccatt gcaaataccg attacaacaa cgtcgggtgaa	3480
gccttggtatg cgctcgataa taacgcgctg ctgtgggatg aagacgcagg tgccataaac	3540
gccagccatg atggcaatgc cagcaaaatc accaacgttg cggctggtga tctctccaca	3600
accagtaccg atgctgttaa cggttcccag ttaaacgcaa ccaatattct gggtacgcaa	3660
aatagccaaa tgattaacca gcttgctggt aacactagcg aaacctacat cgaggaaaac	3720
ggtgcgggta ttaactatgt acgtaccaac gacagcggct tagcgttcaa cgatgccagc	3780
gcttcaggta ttggcgctac agctgtagggt tataacgcag ttgcctctca tgccagcagt	3840
gtagccatcg gtcaggacag catcagcgaa gttgatacgg gtatcgctct gggtagcagt	3900
tccgtttcca gccgtgtaat agttaaaggg actcgtaaca ccagcgatc ggaagaagg	3960
gttggtgattg gttatgacac cacggatggc gaactgcttg gcgcgttgtc gattggtgat	4020
gacggtaaat atcgtaaat catcaacgct gcggatgggt ctgaagccca tgatgcggctc	4080
actgttcgcc agttgcaaaa cgccattggt gcagtcgcaa ccacaccaac caaatactat	4140

caccgccaact caacggctga agactcactg gcagtcgggtg aagactcgct ggcaatgggc 4200
 gcgaaaacca tcgttaatgg taatgcgggt attggtatcg goctgaacac gctgggtctg 4260
 gctgatgoga tcaacggtat tgctatcggt tctaacgcac gcgcaaatca tgccgacagc 4320
 attgcaatgg gtaatgggtc tcagactacc cgtgggtgogc agaccaacta cactgcctac 4380
 aacatggatg caccgcagaa ctctgtgggt gagttctctg tcggcagtga agacgggtcaa 4440
 cgtcagatca ccaacgtcgc agcagggttcg gcggataccg atgcgggttaa cgtgggtcag 4500
 ttgaaagtaa cggacgcgca ggtttcccag aataaccaga gcattactaa cctgaacact 4560
 caggtcacta atctggatac tcgcgtgacc aatatcgaaa acggcattgg cgatatcgta 4620
 accaccggta gactaagta cttcaagacc aacaccgatg gcgcagatgc caacgcgcag 4680
 ggtaaagaca gtgttgcatg tggttctggt tccattgctg ccgctgacaa cagcgtcgca 4740
 ctgggcacgg gtcccgtagc agacgaagaa aacaccatct ctgtgggttc ttctaccaac 4800
 cagcgtcgta tcaccaacgt tgctgccggg gttaatgcca ccgatgcggg taacgtttcg 4860
 caactgaagt cttctgaagc agggggcggt cgctacgaca ccaaagctga tggctctatc 4920
 gactacagca acatcactct cgggtggcggc aatagcggta cgactcgcat cagcaacggt 4980
 tctgctggcg tgaacaacaa cgacgcagtg aactatgcgc agttgaagca aagtgtgcag 5040
 gaaacgaagc aatacaccga tcagcgcagtg gttgagatgg ataacaaact gtccaaaact 5100
 gaaagcaagc tgagtgggtg tatcgcttct gcaatggcaa tgaccgggtc gccgcaggct 5160
 tacacgccgg gtgocagcat ggctctatt ggtggcggta cttacaacgg tgaatcggct 5220
 gttgcttttag gtgtgtgat ggtgagcgcc aatgggtcgtt ggggtctacaa attacaaggt 5280
 agtaccaata gccagggtga atactccgcc gcactcgggt ccggtattca gtgg 5334

<210> 101

<211> 681

<212> DNA

<213> Escherichia coli

<400> 101

atgaacctaa agaaaacact gttaagcgtg ttaatgatat tgcaactttg cttattggta 60
 ggggtgtgact atattgaaaa agcgagtaag gtcgacgac tcgttacaca gcaagagttg 120
 caaaaaagca aaattgaggc gcttgaaaaa caacaagaac tcgacaagcg caagatagaa 180
 cactttgaaa aacaacaaac taccatcata aacagtacca aaacgctcgc tgggtgtgggtg 240
 aaggcagtta aaaacaaaca ggacgaatgt gtctttacag aatttaaccc ggcacaaacc 300

187

caatacttta ttttaaataa cggctctgtt ggtttggcag ggaaaataact gtctattgac	360
gcagtagaaa acggcagtggt tattcgtatt tcaactggta acttattaag tgttcctgta	420
tcaaataatgg gtttctacgc aacatggggg ggagaaaaac ccaccgacat caacgcatta	480
gcaaaatggc agcaattgct atttagtacc gcaatgaact cctccctgaa attattacca	540
ggtcaatggc aagacattaa ttgacgcta aaagggtgtct cgoccaacaa cctcaaatat	600
ctgaaattag ccatcaacat ggcaaatatt cagttcgacc gtottcaacc tgctgaatct	660
ccacagcgga aaaacaaaaa a	681

<210> 102

<211> 3327

<212> DNA

<213> Escherichia coli

<400> 102

atgaaaagag ttgtgcgtct tttgggtgtg gggttactgc tccttgttgt gttgttgctc	60
attttgtttg ttctggctca gaccacaccg ctgatatcag cacaggatga gcatgctgtc	120
tggcttcgtc tgttgataac agcgattgtg atctgtttgc taagtatgtg catatttttc	180
ctcttttctt tccggcagaa cgaagcctcg acgatatcac tatacgtca accgactgat	240
ataaaggaaa taaatacggg gcagccgaac tatgcatcac tgctgacgat atatttacgc	300
gaccgctacg gtccgttctg gcgccgtaaa gtccgcctgc tgctggtgac cggcgagcct	360
gaacaggcag aagccatcgc gccgggggtg accgggcaac actggctgga aggcgaccac	420
acggtgctga tatatggcgg caggccaaca gcggagcctg atgtcacact gctgaccgcc	480
ttaaaaaaac tgcgccgcag ccgtccgtg gacggcatca tctgggcgct gacagaagaa	540
cagagccgcc agacagcgca actcgacaaa ggctggcgcg gactgataaa cggcggttaag	600
cgactcggtt ttcaggctcc actctatattg tggcagggtct gtgacgacgg tgattatcag	660
accggacgcc ccctgcaaag cgtcggctgc ctgctgccgg aacgctgtac cccggaacaa	720
ctggctgtaa tgctggaagc agccgctgac ggaacagggc atgtcgcagc tactgaccga	780
taccgcatgt tttctgctgc gtctggctca tacccttgca gagcggggta ttgctcactg	840
gcagaccgtc ctgaaaccgc tgctggcagg cggcgcatct tcttccctgc gcctgcgcgg	900
cctgatgttc agcccgcgc ttgccgccgt gccggaggcc agcacctcat gcagtggctg	960
ccgtcaccgg tctgggcggg cgtgacggtg ataacgcgcg cgggcgcacg gtgggttttc	1020
ctgtggctgc gtaccgcaact gatgtccgct gtctgcgtgc tggatgatg gggggccgga	1080
atgacgacct cgttcttcgc caaccgcgct cttgttcagg aaaccggtat ccagacggca	1140

cgtgcgcttg ataccgcgct gccgctggca gaacaactgg tggcgctgca taccctgcag	1200
ggcgaactgg aacgcctgca atatcgatc cggaagggtg cgccgtggta tcagcgtttt	1260
ggccttgaac gtaaccaaca actgctcgcc gccgcttttc ccggctatgc gcaggcggca	1320
aaccggctgg tgcgcgacgt ggccgttgac catctgcaac agcaactgaa cgcctttgtc	1380
gccctgccc ccaacagtcc tcagcgatc gccaccggtg aacaacgcta taagcagctt	1440
aaggcattgc tgatgacttc ccgcccggaa aaggccgacg ctgccttttt cagtaccacg	1500
ctgatggcgg acggtctgcg ctacgagaat atcccgaag gtgtgcggca gagcggtgtg	1560
ccgtcactgc tgaccttctg gacggcgaac ctgccggaac acccgcatg gaaaacatcg	1620
ccgccaccgg aactgaccgg cgcagtgcgt aaaatcctgc tgcgccagat tgggtgtgcgt	1680
aatgccgaaa acacctcta ccagaacgtg ctgcaacagg tgtcccgcaa ctacgccgat	1740
atgacgctgg cggacatgac cggggatacc ctaccgaat ctcttttcag tacggaacag	1800
acggtgccgg ggatgttcac ccgtcaggcg tgggaaggac aggtcaggga agccatcgag	1860
cagggtgtga cggcgcggcg cgaggaaatc gactgggtac tcagcgaccg ccagcaggat	1920
acctctgcgg atatctcgcc ggatacgtg cgtaaccgtc tcacctcacg ctactttacc	1980
gactttgccg gaagctggct ggcgtttctc aacagcattc actggaaaaa ggaagactcg	2040
ctctccggca ttctcgacca gctgacactg atggccgatg cccgtcagtc gccactgatt	2100
gcgctgacgg acacctcgc gtggcaggcg gcgacaggca gggaaaaccg tggctctgtca	2160
gactcgctgg cgaaatcggc acaggaactg ttaacggca aggagaaaac gccgcagcaa	2220
tcccgtaag gtgacgacgt gcctgtcggg ccgctggata aaaccttcac gccgctgctg	2280
cgtttgctgg gcgataaggc cggaggcggc gacagccagc tgagtctaca gacctacctc	2340
accgcgtca cccgcgtgcg cctcaaaactg caacagggtg ccaacgcccc cgaccgcag	2400
gagatgaccc aacaactggc gcagacggtc ttacagggtg aaaccgttga cctcaccgac	2460
accgcgact acggacggtt aatcgccgcc agtctgggcg aagaatggag tggcttcggt	2520
caggcgctgt tcgttcgccc ggtagagcag tcgtggcggc aggtgctgac gcctgcggcg	2580
gacagcctga accgccagtg gcagcgggcg attgtcagcc actggaatca ggacttcgct	2640
ggccgctatc cgttcaaagc ctcacagaac gatgcctccc tccccctgct ggcgagctac	2700
ctgcgcgatg acgggcgcat caacctgttt atcgccgcca acctttccgg cgtgctgaaa	2760
cgagagggcc gctactgggt ggctgacgcc atgaacacgc aggggctgac ggtcaatccg	2820

189

gactttatcc ggcacctgaa ccgcctgcgc gacgtggccg ataccgcctt tgccagcggc 2880
 gatgccggga tacattttga actgcgggca aaaccggcgc gtgacgtgat gaagacgcat 2940
 ctggtgattg acgggcagga gctggaatat ttcaaccaga aagaacgctg gcagcgTTTT 3000
 aactggccgg atgaacagtg gcaaccgggc gcatcgctaa gctggaccag cacacaggcg 3060
 atggagcgca tactggcgga ttaccgggga agctggagtc ttattcgctt gctggaacag 3120
 gcgcaggatga cgccgggtga cagcagcacc ttttaagggtg tgtggaaagc gcaggacggc 3180
 ctgccgctga attacctgct acgggttgaa cagggttaaag ggccgctggc gctgctggag 3240
 ctgaaaaact tccgcctgcc gggacagggtg tttctgaccg gaaaaagtat gaaggatgtg 3300
 gaagagtatg gggaagacgc cgatgag 3327

<210> 103

<211> 534

<212> DNA

<213> Escherichia coli

<400> 103

atgtttccta ttcgttttaa acgtccggcg ttgctctgta tggcgatgct gacggttgtt 60
 ctgagtggct gcggcctgat tcagaaagtg gtggatgaat cgaaaagcgt ggccctcagcc 120
 gttttctaca aacaaatcaa aatactgcat ctcgatttct tctcccgag cgccctgaat 180
 acggatgcgg aagatacgcc gctttccacg atggtgcatg tctggcaact gaaaaccgcg 240
 gaagattttg acaaggcgga ttacgacacc ctgtttatgc aggaagagaa gacgctggag 300
 aaggacgtac tggcaaaaca caccgtctgg gtaaaaccgg aaggcacggc atccctgaat 360
 gtgccgctgg ataaagagac gcagtttgtc gccattattg ggcagtttta tcaccctgat 420
 gaaaaaagcg acagctggcg tctggtgatc aaaaggagcg aactggaggc cgacaagccg 480
 cgctcgattg aactgatgag aagcgacctg cgactgctgc ctctcaagga taaa 534

<210> 104

<211> 840

<212> DNA

<213> Escherichia coli

<400> 104

atgatttcag ggggaaatat gttgaaagaa tggatgatat ttaogtgcag tttattgact 60
 ctggctgggg cgtcactgcc cctcagtggc tgtatttcca gaggccagga gtctatatcc 120
 gaagggggcg catttggggc agggatcctg cgcgaaaccg gagcaacaaa aaaagccgac 180
 acgaaagacc tcaatgtgcc accaccggtt tatgggtccg cgaggtgat atttcgcatt 240
 gatgacaacc gctatttcac gctagaaaat tataccact gcgagaacgg gcagacgttt 300

tataataata aagcaaaaaa cattcatggt aaaatattag acgcttcagg gtattttattt 360
aaaggccgct tattctgggt atcaacgcgt gatgattttc tggcctttcc tgccacgtta 420
aataccagac acgcttcctg tatgggggtcg aataaaggct gtatgaatgc ggtcattgtc 480
actaccgatg gtggaaaaag acgcagtgggt gtgccatacg gcagttatac ccagaatccg 540
accggtgcca cgaggggatta tgacatgctg gtgatgaatg acggcttcta cctgcttaga 600
tatcgggggg gacagggcag atttagtccg gtgatactta gatggattct cagtactgaa 660
gatagctctg gtgttggtcg ttcagaagat gcttatgaat tgttccgtcc cggagaagag 720
gtaccctcca ccggttttta taaaatcgac ctgtcacgtt tttatcccaa aaacaacgtt 780
atggaaatgc agtgtgacag gacgctggag ccagttcaac cttcagagag taaaattcaa 840

<210> 105

<211> 1503

<212> DNA

<213> Escherichia coli

<400> 105

atggaacacg ttagcattaa aacattatat catctcctgt gctgtatgct gctctttatt 60
tccgctatgt gcgctttggc gcaagaacat gagcctatcg gggcgcaaga tgagcgctg 120
tcgacattaa ttcaccaacg gatgcaggag gccaaggtcc cagccctttc cgtaagtgtg 180
accattaagg ggggtacgtca gcgatttgct tacgggtgtg ccgatgtggc tagtcagaaa 240
gcgaatactc tagacacagt ttacgagctg ggatcgatga gtaaggcgtt taccggactt 300
gtgggtgcaaa tactgattca ggaaggcaga ctccggcaag gggatgatat cattacctat 360
ctgccggaaa tgcgcttgaa ttatcagga aaacctgctt ccctgaccgt ggctgatttc 420
ctttatcata catcaggatt gcctttttca aactggctc ggctggaaaa ccctatgcct 480
gggagcgctg tggcacagca actgcgcaac gagaatctgc tgtttgcgcc ggggtgcgaag 540
tttagctatg cctccgcaa ttatgatgtg ttgggcgagg tgattgaaaa tgtgacggga 600
aaaaccttta cagaggtcat tgcggaacga ctacgcagc cgctgggcat gtcggcgact 660
gtggcagtta agggggatga gattattgtc aacaaggcaa gcggctataa actgggattc 720
ggcaaaccgg ttctgtttca tgcgcctctg gccgggaacc atgttcctgc cgctatatc 780
catagcactc tgctgatat ggaaatatgg atagacgcct gggtgcacag aaaggctttg 840
ccggcaacgc tgcgtgagge gatgagtaac agttggcgtg gtaatagtga tgttccgctt 900
gccgcagaca atcgatcct ctatgccagc gggttggttta tcgaccagaa tcaaggccct 960

191

tacatcagtc acggtgggca gaatccaaac ttttcttctt gcattgcgtt gcgaccggat 1020
cagcagattg gcattgttgc gctggcaaat atgaattcga atctgatact acagctttgc 1080
gcgatatacg ataattatct gcgcattggc aaatatgctg acggcgctgg tgatgcaatt 1140
acagccaccg ataccctttt cgtctacctc acgttggtgc tgtgtttttg gggggcggtg 1200
gttgtagtgc gcggtgcttt ccgtgtttat cgcgcaacgg cgcattggccc tggaaaacag 1260
cagagggttac gtttacgcgt acgtgactat atcatcgcc tggcggttcc tgggctcgtg 1320
gccgccatgc tctatgtcgc accgggtata ctatctccag gacttgactg gcgttttatac 1380
ttggtatggg gtccatcgag cgtgttggcg ataccgttcg gaattatcct gttagctttc 1440
gttctgacat taaatcatca aattaaacga attctattac acaacaagga gtgggacgat 1500
gag 1503

<210> 106

<211> 2046

<212> DNA

<213> Escherichia coli

<400> 106

atgaagaaca aatatatcat tgctccgggc attgcggtga tgtgttctgc agttatatca 60
tcagggttatg ccagttctga taaaaaagaa gatacgcttg ttgttactgc ctccgggttc 120
actcagcagc tcagaaatgc cccggccagt gtctcagtoa ttacttcaga acaactgcaa 180
aaaaaaccgg tttcagatct ggtcgatgca gtaaaagatg ttgaagggat tagtatcact 240
ggtgggaatg aaaaaccgga tatcagtata cgtggtctaa gtggcgatta cacgctgatt 300
ctggtcgatg gacgacgtca gagcggtcgg gaatccagac caaacggcag cggcggtttt 360
gaagccggat ttatccctcc tgtggaagca attgaacgca ttgaagtgat ccgtggccct 420
atgtcttccc tgtatggttc tgatgccatc ggaggggtca ttaatatcat aaccaaacca 480
gttaataacc aaacatggga tggcgactt ggacttgggg ggattattca ggaacatggg 540
aaatttggtg actcaaccac aaatgacttc tatctgtcag gccattgat taaggataaa 600
cttgggtcttc agctatatgg aggaatgaac tatcgcaagg aagatagtat ctctcaggga 660
acaccggcaa aagataataa gaatataacg gcaacgctcc agtttactcc gactgaaagc 720
cagaagtttg tttttgaata tggaaaaaat aaccagggtc atacattaac acctggtgag 780
tctctcgatg cctggactat gcggggaaat cttaacaac caaacagtaa aagagaaacg 840
cataattcac gtagtcactg ggtagcagca tggaatgcc agggcgaaat actgcacct 900
gaaattgctg tttatcagga gaaagttatt cgtgagggtta aatcaggtaa aaaagataaa 960

tataatcatt gggatcttaa ttacgagtca agaaaaccgg aaataaccaa cacaatcata 1020
gatgcaaaag tgacggcatt tctgccggaa aatgtactga ccatcggagg tcaatttcag 1080
catgcagagc tccgtgatga ctccagccacg ggtaaaaaaa cgacagaaac acagtctggt 1140
tcaattaaac agaaagctgt ttttatagaa aatgaatatg cagcaacgga ttctctcgcc 1200
ctgactggag gactgctgtc cgataatcat gaaatctatg gcagttactg gaatccaaga 1260
ttgtacgctg tttataacct gaccgataat ctccactca aaggggggat cgcaaaagca 1320
tttcgggctc cttcaattcg tgaggtagt cctggatttg gaacactgac gcagggtggt 1380
gcctctatta tgtatggaaa caggacctg aaaccggaga ccagtgtaac cgaagagatc 1440
gggtattattt atagtaatga tagtggtttt tccggcagcg cgacgctggt taatactgat 1500
tttaaaaata agttgaccag ttacgatata ggtacaaaag atccagtcac cgggttaaac 1560
acttttattt atgataatgt aggtgaggca aatatcagag gggaggagct tgcaactcag 1620
attcctgtgt atgataaatg gcatgtatct gcaaactata catttactga ctctcgtcga 1680
aaaagtgatg acgaaagtct caatggcaag tcgctgaaag gggaacctct ggaaagaact 1740
cccagacatg cagccaatgc aaaactggaa tgggattaca ctccagatat tacattttat 1800
tcctctctga attatacggg aaaacaaatc tgggcagcac aaagaaatgg tgctaagggt 1860
ccccgcgttc gtaatggatt cacatctatg gatattggtc taaattacca gattctgcc 1920
gacacgctga ttaattttgc cgttcttaac gtcacagaca gaaagagcga ggatatcgat 1980
accattgatg gtaactggca ggtcgatgaa ggacgccgtt attgggctaa tgtaagagta 2040
tccttc 2046

<210> 107

<211> 492

<212> DNA

<213> Escherichia coli

<400> 107

atgggggttta gaaaaacaat aatcacttcg gtaggtttga tatttatttc attctctttt 60
gtggcaaagt gctctcaact caaaaatttg aataattact cagtgatgct ttgtggaaaa 120
gtgtcaaata atatcctgga tgatattggg ggttataaag aaagaaatat attaagtctg 180
cgagctataa aaaaaatcat aataatgaca atcgtaaata ttatatTTTT ctattccttt 240
caatcgactg cggatgaaat ggttttaata aaaaaatacg ggtttgggct tgagagagat 300
atcaaaggaa ggccattaat ttatcctatc gaaaattatg atgagtgtaa gaaaaaatgc 360

aatcatatga attatatagc ggatgtcaat gctcaattag ctatgagtaa aaaaaataac 420
 aggatttttg ctaacataac ctttactaac aatagctcta ccacgtattt ttttctaaat 480
 attatctacc ta 492

<210> 108

<211> 654

<212> DNA

<213> Escherichia coli

<400> 108

atgaatcaaa ttaaagataa taaggtaatt atgaaaataa aaaatttaat atcagtcatt 60
 ttactatcag gaggtattat ggggactgga ttgtactcga gcgataacca tcaaaaaatc 120
 cgcagcaggt ttaatatata ggaatcatat tgtgccatta agactaatgg tgtccttgga 180
 ttcagcaacc gaaaggatgt attgcgagaa aatgggtgatt caaccggaac caccagttcc 240
 agcactaatg ccatgatgct gatggaaaat ggtgaaaatg aaatcagtct ggagattggg 300
 gcgttaaggt ggttttctga taaacctgcc agtaccgaag aacgagggca tttctcccaa 360
 aaagcagggg gcagtctgga tttgggttcgt tttgttaagc aggaagaaac catactttct 420
 tcgataaagg tgaccatcaa ccagcagga atacctgaag cgcagccaga cagcatgcat 480
 cctgttatcc gaaaagagat tctggctgag caggcagaac ccggatttat tgatccagac 540
 tattttaatg aaacttattt cccgaaaggg atgaagggtg atcaatttac acaaaaggtc 600
 tcggtggcgg ggcttcctga tgggcctgga cgcagtagcg cttttaccgg agca 654

<210> 109

<211> 8198

<212> DNA

<213> Escherichia coli

<400> 109

atgcatcagc ctcccgttcg cttcacttac cgctgctga gttacctggt cagtgcgatt 60
 atcgccgggc agccgttggt accggctgtg ggggccgtca tcacccaca aaacggggcc 120
 ggaatggata aagcggcaaa tgggtgtgccg gtcgtgaaca ttgccacgcc gaacggggcc 180
 gggatttcgc ataaccggtt tacggattac aacgtcggga aggaagggtt gattctcaat 240
 aatgccaccg gtaagcttaa tccgacgcag cttgggtggac tgatacagaa taaccggaac 300
 ctgaaagcgg gcggggaagc gaagggtatc atcaacgaag tgaccggcgg taagcgttca 360
 ctgctgcagg gctatacggg agtggccggc aaagcggcga atgtgatggt tgccaacccg 420
 tatggtatca cctgtgacgg ctgtggcttt atcaacacgc cgcacgcgac gctcaccacg 480
 ggcaaacctg tgatgaatgc cgacggcagc ctgcaggcgc tggaggtgac tgaaggcagt 540

atcaccatca atggcgcggg cctggacggc acccgagcg atgccgtatc cattattgcc 600
cgtgcaacgg aagtgaatgc cgcgcttcat gccaaggatt taactgtcac tgcaggcgct 660
aaccgtgtaa ctgcagatgg tctgtgcaga gccctgaagg gccaagggtga tgtgccgaaa 720
gttgccgttg ataccggcgc tctcggtgga atgtacgcca ggcgtattca tctgacctcc 780
actgaaagtg gtgtcggggg taatcttggg aacctttatg cccgcgatgg cgatatcacc 840
ctggatgccg gcggcagact gactgtcaac aacagtctcg ccacggggggc cgtcactgca 900
aaagggtcagg gcgtcacctt aaccggcgac cataaagcgg gaggtaacct gagcgtcagc 960
agccggagag atatcgcttct cagcaatgga acgcttaaca gcgacaagga cctcagcctg 1020
accgccggcg gcagaatcac tcaacagaat gaaaaactga ctgccggccg ggatgtaacg 1080
cttgccgcga aaaacatcac acaggatacc gccagccaga ttaacgcggc ccgcgatatc 1140
gtgactgtcg ccagtgcac gctgacaaca caggacaga taaccgccgg gcagaatctc 1200
acggccagcg ccaccacgct gacgcaggac ggaatattgc tggcgaaaag tcatgcggga 1260
ctcaatgcgc gtacgctgaa taacagtggc gcgcttcagg gagctaccct gacgctcggc 1320
agtacaacgc tcagcaacag tggtccctg ctcagtggcg gtccoctgac catgaatacc 1380
cgcgacttta ccagagcgg ccgcactggc gccaagggca aagtggatat catggccagt 1440
gggaaaactga ccagtacagg tttgctggtg acgatgcact tgggtgctgaa ggcgaggat 1500
gtgacacaga acggtgtgct gtccggcggc aaagggctga cggtcagtgc gacgagctcc 1560
ggtaaaaaat cggtcaccca cagcgatgct gcgatgacgc tgaatgtgac aacagtggcg 1620
ctggacgggg aaaccagtgc cggtgacacc ctccgggttc aggcagacaa actgagtacc 1680
gcagcggggc cacaacttca gagcggcaaa aatctcagca tcaacgccag agatgcacgt 1740
cttgaggta cgcaggcagc acaacagacc atgggtggtga acgccagtga aaagctcacc 1800
cacagcggga aaagcagtgc cccgtcgctc agcctcagt gcgcggaact gaccagcagc 1860
ggcgactttg ttggttccgc cctgaataca cagtcacaga ccctgaccaa cagcgggtctg 1920
ttgcaggggg aggcctcact caccgttaac acacagaggc ttgataatca gcagaacggc 1980
acgctgtaca gtgctgcaga cctgacgctg gatataccgg acatccgcaa cagcgggctt 2040
atcacccgtg ataatggttt aatgttaa atgtgtctccc tcagcaatcc gggaaaaatc 2100
atcgctgaca cgctgagcgt caggcgacc acgctggatg gtgacggcct gttgcagggc 2160
gccggtgcac tggcgcttgc tggcgacacc ctctcacagg gtagtcacgg acgctggctg 2220

acggcgagc acctctccct ccggggcaaa acactgaata ccgcagggac cacgcagggga	2280
cagaatatca ccgtgcaggc ggacagatgg gcgaacagtg gttccgtgct ggcaaccgggt	2340
aaccttactg cttcggcaac cggtcagttg accagtaccg gcgatatcat gagccaggggt	2400
gacaccacgc tgaaagcagc caccacggac aaccgggggca gtctgctttc ggccggcacg	2460
ctctcccttg atggaaattc actggataac cgcggcactg tccagggtaa ccatgtcacg	2520
attcgccaga acagtgtcac caacagtggc acgctcaccg ggatcgccgc actgacgctt	2580
gccgcccgtg tggcatcccc tcaacctgcg ctgatgaata acggaggttc attgctgacc	2640
agcggcgatc tgacaatcac cgcaggcagt attaccagtt ccggacactg gcagggcaaa	2700
cgggtgctga tcaccgcaga cagtctggca aacagcgggg cgatccaggc ggctgacagc	2760
ctgactgcac gtctgacggg tgagctcgtc agcacagcgg gcagcaaagt cacctcgaac	2820
ggtgaaatgg cgctcagtgc actgaattta agcaacagcg gacaatggat tgcaaaaaat	2880
ctgaccctga aggcgaactc actgaccagt gggggtgaca tcaccggtgt ggatactctc	2940
acgctcacgg tgaatcagac gctgaacaat caggcgaacg gaaaactgct cagtgcaggt	3000
gtgctgacgc tgaaggcaga cagtgtcaca aacgacgggc aattacaggg aaatgtcacc	3060
accatcacgg caggacaact caaaaacggc gggcatctgc agggcgaaac gctgacgctg	3120
acagcctccg gtggcgtaga caaccgttcc ggtgggtgttc tgatgagccg gaatgcactg	3180
aatgtcagta ctgcgaccct gagtaaccag agcacgatac aggggtggagg cggggtttcc	3240
ctgaacgcca cagaccgtct gcagaacgac ggcaaaatcc tctccggcag taacctcacg	3300
ctgacggcgc aggtgctggc gaacaccggc agcggactgg tacaggctgc caccctgctg	3360
ctggatgtgg tgaatactgt caacggcgga cgcgtacttg ccaccggcag tgacgttaaa	3420
ggaaccacgc tgaataatac cggtagcctt cagggtgcga ctctggtgaa ttaccacaca	3480
ttcagcagcg gtaccctgct gggaacctcc gggcttggcg tcaagggcag ttcactgctg	3540
caaatggta cagggcggct gtacagtgca ggcaacctgc tgcttgacgc tcaggacttc	3600
agtggtcagg ggcaggtggg ggccaccggg gatgtcacac tgaaactgat tgctgcoctc	3660
acgaatcatg gtacctggc cgcagggaaa acctttccg tcacgtcgca aaatgccatc	3720
accaacggcg gtgtcatgca gggatgatgc atggtgctcg gtgccggaga ggcattcacc	3780
aacaatggac tgactgccgg taaaggcaac agtggttttca gcgcacagcg tcttttcctt	3840
aacgcaccgg gttcacttca gggcggtggc gatgtgagtc tgaacagccg gagtgatata	3900
accatcagtg gttttaccgg cacggcaggc agtctgacaa tgaatgtggc cggtagcctg	3960

ctgaacagtg cgctgattta tgcggggaat aacctgaagc tgtttacaga ccgtctgcat	4020
aaccagcatg gtgatatcct ggccggcaac agtctgtggg tacagaagga tgcttccggc	4080
ggtgcaaaca cagagattat caataattcc gggaatattg agacgcatca gggcgatatt	4140
gttgtaagaa ccgggcatct tctgaaccag cgggagggat tttctgccac aacaacaacc	4200
cggactaacc cctcatccat tcagggaatg ggaaatgctc tggttgatat tcccctttcc	4260
cttcttctctg acggcagcta tggctatttc acccgtgaag ttgaaaatca gcacggtacg	4320
ccctgcaacg ggcacggggc atgcaatc acaatggata cgctttatta ttacgcgcgcg	4380
tttgctgaca gtgccacaca gcgctttctc agcagccaga acatcacaaac agtaaccggt	4440
gctgataatc cggcaggccg cattgctca gggcgtaatc tttctgctga ggctgaacga	4500
ctggaaaacc gggcgctatt tatcctggcg aatggggata tcgcactctc gggcagagag	4560
ttaagcaatc agagctggca gacggggaca gagaatgaat atctgggtata ccgctacgac	4620
ccgaaaacgt tttacggtag ctatgcaaca ggctctctgg ataaactgcc cctgctgtca	4680
ccggaatttg aaaacaatac catcagattt tcaactggatg gccgggaaaa agattacacg	4740
cccggtaaga cgtattattc cgttattcag gcggggcggg atgttaagac ccgttttacc	4800
agcagtatca ataacggaac aaccactgca catgcaggta gtgtcagtcc ggtggtctct	4860
gcacctgtac tgaatacgtt aagtcagcag accggcggag acagtctgac acagacagcg	4920
ctgcagcagt atgagccggt ggtggttggc tctccgcaat ggcacgatga actggcagg	4980
gccctgaaaa atattgccgg aggttcgcca ctgaccggtc agaccggtat cagtgatgac	5040
tggccactgc cttccggcaa caatggatac ctgggtccgt ccacggaccc ggacagtccg	5100
tatctgatta cggngaacc gaaactggat ggtctcggac aggtggacag ccatttgttt	5160
gccggactgt atgagcttct tggagcgaag ccgggtcagg cgccacgtga aacggctccg	5220
tcgtataccg atgaaaaaca gtttctgggc tcatcgtatt ttcttgaccg cctcgggctg	5280
aaaccggaaa aagattatcg tttcctgggg gatgcggtct ttgatacccg gtatgtcagt	5340
aacgcggtgc tgagccggac gggttcacgt tatctcaacg gactgggttc agacacggaa	5400
cagatgcggt atctgatgga taacgcggcc agacaacaga aaggactggg attagagttt	5460
ggtgtggcgc tgacagctga acagattgct cagcttgacg gcagcatact gtggtgggag	5520
tcagtcacca tcaacggaca aacagtcag gtcccgaaac tgtatctgtc gccggaagat	5580
atcacccctgc ataacggcag cgttatcagc gggaacaacg tgcaacttgc gggcggcaat	5640

atcaccaaca gggcgggcag catcaacgca cagaacgacc tctcgctoga cagttccggc	5700
tatatcgaca acctgaatgc ggggctgata agcgcgggcg gtagcctgga cctgagcgcc	5760
atcggggata tcagcaatat cagctcagtc atcagcggtg aaaccgtaca actggaaagc	5820
gtgagtggca acatcagcaa tatcacccgg cgtcagcaat ggaatgcggg cagtgcacgc	5880
caatatggtg gtgtgcatct cagcggtacg gacaccggtc cggttgacgac cattaaaggc	5940
actgattcac ttctcgctgga tgcagggaaa aacattgata ttaccggggc aacgggtctcg	6000
tccggtggag accttggaat gtctgcgggt aatgatatca acattgccgc aaacctgata	6060
agtgggagca aaagtcagtc cggtttctgg cacactgatg acaacagttc atcatccacc	6120
acctcacagg gcagcagcat cagcgccggc ggtaacctgg cgatggctgc aggccataat	6180
ctggatgtca cggcatcctc tgtttctgcc gggcacagcg ccttgcttctc ttgcagggtca	6240
cgacctagtc ttgaatgcag tcagggaaaa gcaaaaacaa gtcgcaacgg caggtcagaa	6300
agtcatgaaa gccacgcagc tgtgtccacg gtgacagcgg gcgataactt cctccttggt	6360
gccggtcgtg atattgccag tcaggctgcc ggtatggctg cggaaaataa cgtgggtcatc	6420
cggggcggac gtgatgtgaa cctgggtggca gagtctgccg gcgcaggcga cagctatacg	6480
tcgaagaaaa agaaagagat taacgagaca gtccgtcagc agggaaacgga aatcgccagc	6540
ggtggtgaca ccacgtcaa cgcaggacgg gatatacccg ctgttgcgtc atccgttacc	6600
gcaaccggca atatcagcgt gaatgccggt cgtgatgttg ccctgaccac ggcgacagaa	6660
agtgactatc actatctgga aacgaagaaa aaaagcggag gttttctcag taagaaaacc	6720
accgcacca tcagtgagga cagtgccacc cgtgaagcag gtcacctgct gtcggggaac	6780
cgcgtagaccg ttaacgcggg tgataacctg acggtagagg gtccggatgt ggtggctgac	6840
cgggatgtgt cactggcggc gggtaaccat gttgatgttc ttgctgccac cagtacagat	6900
acgtcctggc gctttaagga aacgaagaaa tccggtctga tgggtaccgg cggatttggt	6960
ttcaccattg gcagcagtaa gacaacgcac gaccggcgcg aggcggggac aacgcagagt	7020
cagagtgccg gcaccatcgg ctccactgcc ggtaatgtca gtattaccgc gggcaaacag	7080
gctcatatca gcggttcgga tgtgattgcg aaccgggata tcagcattac cggtgacagt	7140
gtggtggttg acccggggca tgaccgtcgt actgtggacg aaaaatttga gcagaagaaa	7200
agcgggctga cggttgcctt ttccggcacg gtgggcagtg ccatcaataa tgcggttacc	7260
agtgcacagg agacgaagga gagcagtgac agccgtctga aagccctgca ggccacaaag	7320
acagcgctgt ctggtgtgca ggccggacag gctgcgacaa tggcctccgc aaccggtgac	7380

ccgaatgcgg gagtcagcct gtcgctcacc acccagaaat cgaaatcaca acaacattct 7440
 gaaagtgaca cagtatccgg cagtacgctg aatgccggga ataatctgtc tgttgctgca 7500
 accggcaaaa acaggggcca taaccgcgga gatattgtga ttgcaggaag ccagcttaag 7560
 gccggtggta acacaagcct ggatgccgag aatgatattc tgttgagtgg cgccgcaaac 7620
 acacaaaaaa caacgggcag gaacagcagc agtggcggtg gcgtgggtgt cagtatcggg 7680
 gcaggtaaag gtgccggtat cagcgccttt gccagcgta atgcggcaaa aggcaggagg 7740
 aaaggtaacg gtactactac cgacaaaacc gtcaccatca acagtggctg ggatacggta 7800
 ctgaacggtg ctgaggtcaa cggcaacagg attatcgccg atgtgggcca cgacctgctg 7860
 ataagcagcc agcaggacac cagtaagtac gacagtaaac agaccagcgt ggctgcccgc 7920
 ggcagtttta cctttggctc catgaccggc tcaggttaca tcgctgcctc ccgggataag 7980
 atgaagagcc gctttgactc cgttgctgaa caaacggaa tgtttgcccg ggtgatgggtg 8040
 gcttcgacat cacagtgggt aaacataccc aactggatgg tgcggtcatt gcctcactgc 8100
 cacaccggag aaaaaccacc tggataccgg acgctgggtt tagtgacttt acaacgaagc 8160
 gggattataa agtcaagtca caggtggaat cagtctga 8198

<210> 110

<211> 963

<212> DNA

<213> Escherichia coli

<400> 110

atgatgttga agaaaacgat atttatatta acgttattct ctggcaacgt aattgctgca 60
 actgtagaat taggttttga aaatgagcaa tataattatg cttatcgttc tgcagatgtc 120
 ttcattgcgt atattaagag taatttcaac cctgttactg attctgcttt gaatgtgtca 180
 ctcacctata tgtatcagga tcaatatggg aaaaaacata aaaaaacatc tgaggacaga 240
 tttaaaacca atcgcgatcg catagagctc tatcttaaag gttatacttt aaatagggga 300
 gcatattctt tttctccttc cgcagggtttc cgttatgagt catgggatgt aaactacgat 360
 aatccgaaaa agcaggataa gtggaaactg gaactacgct tttatcctaa tatgacttat 420
 aaactcaatg accagttaag cctatatatg aatggttttg ttgcccctgt attttttaaa 480
 acacaacaag agtcgagaaa agataacaat tatgtaaagg gtaagttagg ggcgaaacgt 540
 tataacaacg attattatca ggaactccag attctgggtg tcagatataa atttaataat 600
 gataatacgc tctgggcacg agtctataat gaaagaaaat ataataca ttcctcaaaa 660

199

tatgatcgct ggcaattgcg tggaggctat gatttttaaag ttacagagga gtttgttttg	720
agtccattca taagatatga cctctcttat agagaaaaaa acctcgaaag cacaagtaat	780
aatggttttat caaaaaataa taaagaaatt cgaactggag ccagcttttc ctataaaatt	840
atcccttctg taaaactggg aggagaaata tacaggcaaa caaccaacat tgaaaactat	900
tatggagagc attctgaaga caaaaaccgc atgttctaca aacttggtat aaacaaaaca	960
ttt	963

<210> 111

<211> 1761

<212> DNA

<213> Escherichia coli

<400> 111

atgcagcacc ggcagaaaaa cattctgacg aaaacgtccc ttttatcccg tgcgttgtct	60
gtcccctgtt gtgatatgtt cggcgcgggc tctccgtgga tatgctatct ctccctctcc	120
gttttttctg gttgtttcat ccccgcatth tctgtctcgg cagccatgct gtctccgggt	180
gaccgcagtg caattcagca gcaacagcag cagttgctgg atgaaaacca gcgtcagcgt	240
gatgcgctgg agcgcccgt gaccatcacg ccgtctcgg aaacgtctgc cggtaactgaa	300
ggtccctgct ttacgggtgtc aagcattgtt gtcagtgggg ccacccgact gacgtctgca	360
gaaaccgaca gactggtgcc gtgggtgaat cagtgtctga atatcacggg gctgaccgog	420
gtcaccgatg ccgtgacgga cggctatata cgccggggat atatcaccag ccgggccttt	480
ctgacagagc aggaccttc agggggcgta ctgcacataa cggtcatgga aggcaggctg	540
cagcaaatec gggcggaagg cgctgacctt cctgcccga ccctgaagat ggttttcccg	600
ggaatggagg ggaaggttct gaacctgcgg gatattgagc aggggatgga gcagattaat	660
cgtctgcgta cggagccggt acagattgaa atatcgcccg gtgaccgtga gggatggctg	720
gtggtgacac tgacggcatt gccggaatgg cctgtcacag ggagcgtggg catcgacaac	780
agcgggcaga agagtaccgg tacggggcag ttaaattggtg tcctttcctt taataatcct	840
ctggggctgg ctgacaactg gtttgtcagc gggggacgga gcagtgactt ttcggtgtca	900
catgatgcga ggaattttgc cgccggtgtc agtctgccgt atggctatac cctggtggat	960
tacacgtatt catggagtga ctacctcagc accattgata accggggctg gcggtggcgt	1020
tccacgggag acctgcagac tcaccggctg ggactgtcgc atgtcctgtt ccgtaacggg	1080
gacatgaaga cagcactgac cggaggtctg cagcaccgca ttattcacia ttatctggat	1140
gatgttctgc ttcagggcag cagccgtaaa ctcaattcat tttctgtcgg gctgaatcac	1200

200

acccacaagt ttctgggggg ggtcgggaaca ctgaatccgg tattcacacg ggggatgccc 1260
 tggttcggcg cagaaagcga ccacgggaaa aggggagacc tgcccgtaaa tcagttccgg 1320
 aaatggtcgg tgagtgccag ttttcagcgc cccgtcacgg acaggggtgtg gtggctgacc 1380
 agcgcttatg ccagtggtc accggaccgt cttcatggtg tggaacaact gagcctcggg 1440
 ggtgagagtt cagtgcgtgg ctttaaggat cagtatatct ccggtaataa cggcggttat 1500
 ctgcggaatg agctgtcctg gtctctgttc tccctgccat atgtgggaac tgtccgtgca 1560
 gtggctgcac tggacggcgg ctggctgcac tctgacacg atgaccgta ctogtccggc 1620
 acgctgtggg gtgctgctgc cgggctcagc accaccagtg gccatgtttc cggttcgttc 1680
 actgccggac tgctctggt ttaccggac tggcttgccc ctgaccatct cacggtttac 1740
 tggcgcgttg ccgtcgcgtt t 1761

<210> 112

<211> 2220

<212> DNA

<213> Escherichia coli

<400> 112

atgaataagc acacactatt actgactggt ctttttctga atttgatttg tactcccgtt 60
 tttgtcaaa actggcaggt ggcgacgttt ggtcagtcta cggatctcaa cttttcatcg 120
 ctgatagatt cggccaagat cggacggaat aatgcctggc ttgcaggaaa caataatatt 180
 cttgaagctg gaaaatttta cactttacca acagattttt ttattgaaag ccgtggggga 240
 aaaattgcta actcccatga cggatatgacc gtcttttata ctattgttcc ggttactcag 300
 acattccgac tggaggctga tttgacatta gaacagattg gtccggaggt gaatggaaaa 360
 tcaccagcgg gacaggaggg agctggattg tttgtcagag atattatcgg tcctcagcga 420
 caggaaacctc agtcagctgg aacagaagaa tatccccagg cctctaatat attgatgaat 480
 gcctttatta cacagaataa aaagaatgat aacttagtac agattacttc aattgttcgt 540
 gaaggagtaa taaaaacatg gggtaatgaa ggtattacaa ttaagaaaca gccgatcatt 600
 gagaatataa actttacgca aaaaagaaat attcatatga cgatcgagcg actaccagag 660
 aagttcatcc tgaccgcttt tgataccgat cgtaaagaaa atcagtcatg gcaattttct 720
 gattactcag gctttatgaa tcaactggat aataatagtt tagctattgg ttttttgcc 780
 gcacgaaatg cgaaactaag ggtgaaaaat gcatcattta aaccgggcaa gccactgggt 840
 gattacaaac aattaacttc acgtcaattc agtcgtgtcc ggcataaagc ccctgaactt 900

201

```

tttcttgctt cacctcaatc cgttgtaaga aactcaacaa ctcttcaatt tttggccaat    960
caggctggaa tagtcagtat tgataatgat aagcagacta agcaggtgca ggcgggtgaa    1020
ctggtacagt ttccagttac tttgcaaaaa aaacataatg acttcaccgt caactttaac    1080
gttgatggga atatatcaaa aaaagctata cgcàtagagc aggttaaadc aaacctgact    1140
gatccttatg agatttacgt atgtagtgat tgtcgacagg gggccagagg cagcaaaaat    1200
gacctgtag atttacagac agccgtaaaa tttgtcgac ccggcggtaa tatatacctt    1260
aacgatggtc aatatcatgg aattacctta gatcggggaat taagtggaat acctggcaag    1320
tataaaacaa tttctgccat taatccacat aaagccattt ttataaacia gacattcaat    1380
ctggatgcaa gttactggca tctaaaatcc gtggtctttg acggcaatgt ggataatgga    1440
aataataaac cagcatatct gcgtatagct ggtagctata atattattga gcatgtgata    1500
gccagaaata atgatgatac ggggaatttct atttcagcga aagataaaaa ccgttttttc    1560
tggccagctc ataacttagt tttaaactca gattcatata ataactttga tttatccggg    1620
attaatgccg atggttttgc tgcaaaatta ggtgtcggac cgggaaacat ttttcgagga    1680
tgcattgcac ataataatgc agatgatggg tgggacctat ttaacaaaat tgaagatggg    1740
ccaaatgcat ctgttactat tgagaattct gtagcctatg aaaatggcct gccatacaat    1800
aaagcggata tctaaaagg gagtattggc aatggcgggtg aaggtaaac cagtaaatca    1860
caagttatta attccattgc tattaataat aatatggatg gattcactga taattttaat    1920
actgggtcat tgatagttag aaataatata gcaatgaaca atgcacgcta taattatatt    1980
ttaagaacta acccatataa attcccatca tctatccttt ttgataataa ttattcaatc    2040
agagatgatt gggaaaataa aataaaagac ttcttaggtg atacagttaa cagtgtgaat    2100
tataaattgc ttgtttcaca tgaaacagga ccggtacaaa aagatttatt tttcacacga    2160
gatgatagtg gaaatattat ctatcctgat tttttctta atatcattaa taaatttaat    2220

```

<210> 113

<211> 408

<212> DNA

<213> Escherichia coli

<400> 113

```

atgaaaactt ttatcaaaac ttactcgtt gctgtaacta ttctgttctc tgtcttcgct    60
acggcgaaac aagtaaaact gccaaacaac atcaaatagc ttaatactac agaggcgttt    120
tctgtactg agattgacgg tatgaattgc cagacgaaga atccgtttta ctataaagat    180
aacagctatg ttttcgtgct tgaacgtggg ggtgcctggg gttacgacta cactgtctcg    240

```

202

gtacttaacc tgaaaaccgg gaaagcacag atgctcgaat acaaagacaa ccagctgtgc 300
 tcaggtagca acaaaccggt cttcgaaatc aaaaatggcg taccgacggt aggagtcac 360
 gacacatccg gaaaacctgt cgttgtggct ctggacaaac ttaaaacc 408

<210> 114

<211> 675

<212> DNA

<213> Escherichia coli

<400> 114

atgcaattac ctgtaaagtt attaatgagc cttatatctc tggtcagcgt tattgcacgt 60
 gccgggaaat ataaaaatta catccgggat gaaataaaat actggcgata tacatcatac 120
 aagggggggg aatttcggga aggtttcact gatgagaaat tttccagcgc catttacaac 180
 ggaagaatat ttacaatgaa acgtttacat accctgatgt tattttctggc ggttctgttt 240
 actggcttta acgtggaagc agcgagcgtg aaacaagcgc tcagctgcga cccaaacgcc 300
 cgggctgaac aacctggagc gtgtccaaca acgtacgagt tgtacgaagg tgacgctgcc 360
 tacaaagctg cgcttgacaa agcattaaaa ccggtcggac tgagcggcat gttcggtaaa 420
 ggcgggtata tggatggccc tggcggaaac gtaacgccag taaccattaa cggtagagtc 480
 tggctocagg gcgacgggtg caaagccaat acctgaggct gggactttat cgtaaacctc 540
 tataacccaa aaaccatga agtcgttggc taccgctact ttggtttaga tgaccgggcc 600
 tacctggttt ggttcggcga aattggcgtg catgaattcg cgtatctggt gaaaaactac 660
 gtagctgcgg ttaac 675

<210> 115

<211> 2163

<212> DNA

<213> Escherichia coli

<400> 115

atgaaaactc aaataacttt cgctgcgctt ttgcccagcat tagcgtcttt cataccgctt 60
 catgctcatg cctcgtctac ttctgaagat gaaatgattg tcacggggcaa caccgccgcc 120
 gacaccaccg attctgccgc cggtgccggt ttcaaaacga acgatataga tgtcggccccg 180
 ctgggaacga aatcctggat cgaaacacca tattccagca cactgtttac taaagagatg 240
 attgaaaatc agcaggcgca aagcgtcagc gagatgctga aatactctcc cagtacgcaa 300
 atgcaggcgc gcggtggaat ggatgtcggg cgtccgcaaa gtcgggggat gcagggcagc 360
 gtgggtggcca acagccgtct ggacgggctg aatatcgttt caacaaccgc gtttcgggtg 420

gaaatgcttg agcgcacatgga tgtgcttaac agtttgaccg gcgcgctgta cggcccggcg	480
agcccagcag ggcagtttaa ttctgtggcg aagcgcccaa ccgaagagac gctgcgtaaa	540
gtgacgctgg gctatcaaag ccgcagtgcg ttaccggcc atgccgatct ggggtggccat	600
tttgatgaaa acaaacgggt tggctatcgc gtgaacctgc ttgatcagga aggggaaggc	660
aatgtggatg acagcacgct gcgtcgcaaa ctcgtttccg ttgcgctcga ctggaatatt	720
cagccgggca ctacgctaca gctcgacgcc agccattacg aatttatcca gaaaggctat	780
gtcggtagct ttaactatgg gccgaacgtc aaactgccgt ctgcgccgaa tccgaaggac	840
aaaaatctgg cgctcagcac tgcgggcaac gacctcacta ccgataccat cagcactcgc	900
ctgatccact actttaacga cgactggtcc atgaacgctg gcgtgggctg gcagcaggct	960
gaccgcgcga tgcgtagtgt ttccagtaaa atactcaaca atcagggcga tatctctcgt	1020
tcgatgaagg attccaccgc tgcgggacgt ttctgcgtcc tgagcaacac cgccgggctg	1080
aatggtcata ttgataccgg ctctatcggc cacgatctgt cactttctac cacgggatat	1140
gtctggctgc tttatagtgc caaaggaaca ggttcacgct atagctgggg tacaacaaat	1200
atgtatcacc cggatgcgat agatgagcag ggcgatggca aaatccgcac cggcggggccg	1260
cgataccgct ccagcgtaaa tactcagcag agcgttacgc tcggcgatac ggtgacattt	1320
acgccgcagt ggtcggcaat gttctatctc agccagagct ggctgcagac taaaaactac	1380
gataagcacg gtaatcaaac gaaccagggt gatgaaaatg gtttaagtcc gaacgccgcg	1440
ctgatgtata aaattacccc taacacaatg gcctacgtta gctatgccga ttctgtggag	1500
cagggcggta ccgcaccgac ggatgagagc gtaaaaaatg ccggtcaaac gctaaacccg	1560
tatcgagca agcagtatga agtggggcta aaatcggaac tcggcgagat gaatctaggc	1620
gccgcgctgt tccgactgga acgtccgttt gcctatcttg atacggataa cgtgtataaa	1680
gagcagggta accagggtta caacggcctt gagttaaccg ctgccgggaa tgtgtggcag	1740
gggctgaata ttacagcgg cgtgaccttc ctcgaccga aactgaaaga tacggcgaat	1800
gcctcaacca gcaataaaca gggtgtcggc gtgccgaaag tgcaggccaa tctgttggcg	1860
gaatacagtt tgccgtccat accggaatgg gtttacagcg ctaacgtcca ttatacgggc	1920
aaacgcgcgg cgaacgatac caacacctt tacgccagca gctataccac atgggatttg	1980
ggaacgcgtt acaccacgaa agtgagcaac gtcccaacca ctttccgcgt ggtggtaaac	2040
aacgtgtttg ataaacatta ctgggcttct atcttcccat cgggtaccga tggcgataac	2100
ggttcccaa gtgcgtttat cggcggcggc cgcgaagtgc gtgcatccgt caccttcgat	2160

ttc

2163

<210> 116

<211> 2007

<212> DNA

<213> Escherichia coli

<400> 116

```

atgaaaaaca taacgctgtg gcagcggtta agacagggtca gtatcagtac cagcttacgt      60
tgcgcatttc tgatgggggc acttctgacc ctgattgtca gtagtgtcag tctgtattca      120
tggcatgaac aaagctcaca aattcggttac tcgctggata agtattttcc ccgtattcac      180
tctgctttcc ttattgaagg gaacctgaat ctggtggtag accagctaaa tgaatttttg      240
caggctccca acaccacggg gcgattgcaa cttcgtagcc agattattca gcatctcgac      300
accatagaac ggcttagtag gggactgtca tcccgggaac gccacaact gacgggcatt      360
ttgcaggaca gtcgatcact gttatccgag ttggatcgtg cgctttacaa catgttttta      420
ctacgggaaa aggtgagtga gctatcagcg cggattgact ggttacacga tgattttact      480
accgagctta attctttagt gcaggatttc acctggcagc agggaaacgt gctggatcaa      540
atcgccctcc gacagggcga tacggcgcaa tacctgaagc gatctcgtga agtgcaaaat      600
gaacagcagc aggtttatac cctggcacgc attgaaaatc agattggtga cgatctgcgt      660
gacagactca atgagctcaa atcaggacgt gatgacgaca tacagggtgga aactcatctc      720
cgttattttg aaaatctgaa aaaaacggca gatgaaaata tacgtatgct ggatgactgg      780
cctggcacca ttaccctgag gcagaccatc gatgaattgc tggatatggg aatcgtaaaa      840
aacaaaatgc cggatacgat gcgtgaatat gtcgccgccc aaaaagcctt agaggatgcc      900
agtgcacca ggggaagcgac acagggtcgc ttcagaacgt tactggaagc gcagcttggc      960
agtactcatc aacaaatgca gatgtttaat caacgaatgg aacaaattgt tcacgttagc     1020
gggtgggtga tcctgggtgg gacagcactg gcgttactgc ttgcatgggt attcaaccat     1080
tattttatcc gctcacggtt ggtgaaacgc ttaccctac tgaatcaggc cgttgtgcaa     1140
attggtctgg gaggcacgga aacgactatt ccagtttatg ggaatgatga actggggaga     1200
attgcaggat tattacgcca tactctcggc caactcaatg tgcaaaaaca gcaacttgaa     1260
caagaaatta ccgatcgtaa ggtgatagaa gccgatctgc gtgccaccca ggacgaactg     1320
attcagacag caaagttggc ggtagtcggg caaacgatga ccacgctggc ccacgagatc     1380
aatcagccgc taaatgcgct gtcaatgtat ctgtttacag cccgcagggc cattgaacag     1440

```

205

acccagaaag aacaggccag catgatgctt ggtaaagccg aaggggtgat tagtcgtatt 1500
 gacgccatta tccgttccact acggcagttt acccggcgcg ccgaactgga aacatcactc 1560
 catgccgttg atttagcaca gatgttcagt gcggcctggg aacttctggc catgcgtcat 1620
 cgctctctgc aagctacgct tgttctgccc caaggtacag ccacagtttc aggtgatgag 1680
 gtcagaaccc agcaggctact ggttaacgta ctggcgaatg cgcttgatgt ttgtgggcaa 1740
 ggcgctgtca ttaccgttaa ctggcaaata cagggtaaaa cgctgaacgt attcattggc 1800
 gataatggcc cgggctggcc tgaggcattg ttgccttcgt tattgaagcc gtttaccacc 1860
 agtaaagaag taggactggg tattggctct tcaatttggt tgcgttgat ggagcaaagt 1920
 aaaggggaat tgcggctggc atcaacgatg accaggaatg cctgtgtggt actgcaattc 1980
 agactaacgg atgtggaaga tgctaag 2007

<210> 117

<211> 2259

<212> DNA

<213> Escherichia coli

<400> 117

atgaacgtta taaaactggc tatcggctca ggcatattat tgctcagctg cgggtgcttac 60
 tcacaatcca tcagtgaaaa aactaattcc gacaaaaaag gagcggcaga attcagtcgc 120
 ctcagcgttt ctgtcgggaa gacgaccagt gagcaggaag ctctcgagaa aacaggcgcg 180
 accagttccc ggacaacgga caaaaacctg caatcacttg acgcaacagt gcgtagtatg 240
 cctgggtactt atactcaaata agatcctggt caggagagcaa tcagtgtgaa tattcgaggc 300
 atgagcggat ttggctcgtg aaacactatg gtcgatggta ttaccagag tttttacgga 360
 acctctacct ccggaacaac gacgcattgt tcaactaaca atatggctgg cgtacttata 420
 gatcctaact tactggtagc agttgatgtt acacgcggtg acagcagtgg ctctgaaggg 480
 atcaacgccc ttgccggtag tgcaaataatg cgtactattg gcgttgacga tgtaatat 540
 aacggtaata catatggcct tcgttcacgt ttctctgtcg gtagtaatgg gctgggacgc 600
 agcggaatga tcgcccttgg tggaaaaagc gacgctttta cggatacggg aagcattggc 660
 gttatggctg ctgtgagcgg cagttctgtg tactctaatt tctcaaatgg ttctggaatt 720
 aacagcaaag agtttgggta tgataaatat atgaagcaga accccaaatc ccaactgtat 780
 aaaatggata tcagaccaga cgaatttaac agcttogaac tttccgctcg aacctatgaa 840
 aataaattta cacgtcgtga tataaccagt gacgactatt acattaaata tcattacacc 900
 cctttttctg aattaattga ctttaacgta acggccagta ccagtcgcgg taatcaaaag 960

tatcgtgatg gctcgtgta tactttctac aaaacctcag cgcaaaatcg ttctgacgcg 1020
 ctggatatca acaataccag ccggttcact gtcgcggaca atgacctgga gtttatgctg 1080
 ggcagcaaac tgatgcgtac ccgctatgac cggaccattc actcagcggc gggcgacccg 1140
 aaagcgaatc aggaatcgat cgagaacaat ccgttcgcac cctccggcca gcaggatatt 1200
 tcagcgtgt ataccgggct gaagggttac cgcgccatct gggaggcaga tttcaatctc 1260
 aactacacac gtaacaggat cacagggtag aagcccgct gcgattcacg cgttatctgc 1320
 gtgccacagg gtagctacga tattgacgat aaagaggggtg gcttcaacc ttcagttcag 1380
 ctttctgctc aggtaacacc atggcttcag ccgttcattg gctacagcaa atccatgcgc 1440
 gccccgaaca tccaggagat gttcttctct aattcaggag gcgcattccat gaaccattc 1500
 ctgaagcctg aacgtgcaga aacctggcag gcgggtttta acattgatac cagagattta 1560
 ctgggtgaac aggatgcct gcgctttaag gctctggcgt accgcagcag gatccagaac 1620
 tacatctaca gcgagtctta tctggtttgt tctggaggtc gtaaatgcag tctgcctgag 1680
 gtgattggca atggctggga gggcattagc gatgaataca gcgacaatat gtacatctac 1740
 gttaactcgg caagcgacgt tatcgcaaag ggcttcgaac tggagatgga ttatgatgca 1800
 ggttttgctt ttggccgact ctctttcagc cagcagcaaa cagaccagcc aacctccatc 1860
 gccagcacc actttggcgc aggggatata accgaactgc ccagaaaata catgacgctg 1920
 gatactgggtg ttcgcttctt cgataacgcg ttgaccctgg gcactatcat aaaatacaca 1980
 ggcaaggctc gtcgcctgtc gcctgatttt gagcaggacg aacataccgg cgcaataatc 2040
 aaacaggatt tgccgcagat cccaacgatt atcgatctct atgggtactta cgagtacaac 2100
 cgcaacctga cactgaaact ttcggtacaa aacctgatga acagagatta ttcggaggcg 2160
 ctgaataagc tcaacatgat gccaggctctt ggtgacgaga cccaccagc caattccgcg 2220
 cgtggcagaa catggatatt tggcggggac, attcgtttc 2259

<210> 118

<211> 399

<212> DNA

<213> Escherichia coli

<400> 118

atgtcttcga aaacaaatg ctggctatgg atgttactgg tcctcctttc tgaaacctct 60

gcaacatcca cacttaaaat gttcgataac agtgagggga tgacaaaaac gctgctgctg 120

gccctaatacg tcgtactgta ttgcatttgt tactactcgc tttcacgggc agtaaaagat 180

207

atccccggttg gtctggctta cgccacatgg tccggtactg gcattttgat ggtttcaacc	240
cttgggattt tatttttacgg tcaacacccg gataccgccg ccattattgg tatggtcac	300
atagccagcg gtattatcat tatgaatctg ttctcaaaaa tgggcagtga agaggcggaa	360
gaaactccag ttaccaacct cgataaaaaa atcgctaac	399

<210> 119

<211> 858

<212> DNA

<213> Escherichia coli

<400> 119

atgtatataa aaaagcactg gatagcttta tccattctat taataccttg cattggaaac	60
gctcaggaaa ttaaaattga tgaaagctgg ttacatcaaa gcttgaatgt cattggtcgc	120
acagactctc gctttggccc aagactgact aacgacctct accctgaata tactgtagca	180
ggaagaaaag actggtttga tttttatggg tatgttgatc taccgaaatt ctttggcgtc	240
ggcagtcact atgatgttgg gatctgggat gagggtcac cactatttac ggaaatagaa	300
cctcggtttt ccattgacaa attgacogga ttaaatcttg cgttcgccc atttaaagaa	360
tggttcattg caaacaacta tgtctatgat atgggtgaca accagtcac cggcaaaagt	420
acatggtata tggggcttgg tacagatata gacacgggtc taccaattaa gctttctgcc	480
aatatatacg ccaagtatca gtggcaaac tatggtgccg ctaatgaaaa tgaatgggac	540
ggatatacat tcaaaaataaa atatagcaca cctcttaca atttattcgg aggacgattg	600
gtatacaata gttttactaa ctttgatttt ggctccgac ttgcggacaa gtcacacaat	660
aataaacgaa ccagtaatgc tattgcttca agccatatcc tttcccttct atatgaacac	720
tggaaatttg catttacact acgttatttt cacaacggtg gacaatggaa tgcgggagag	780
aaggttaact tcggagatgg tccatttgaa ttaaaaaata caggatgggg aacctatact	840
actattgggt atcaattt	858

<210> 120

<211> 516

<212> DNA

<213> Escherichia coli

<400> 120

atgagaatcg caccgcgtac cttctttgct atttcgccc tggcgtttat tgcgcctcc	60
ggatttagtt tctggcggtt gtcccctgct gaaaatacag ggattatgag ttgttcaaca	120
aaaggcatca tgcgttttga gaatatggaa aaggagaacg ttaacggtaa tattcacttt	180
aactttggca gccagggtaa aggttcgatg gtgctcgaag gctacacgga ctctgccgct	240

208

ggctggctgt acctgcaacg ctatgtcaaa ttacctata ccagtaaagc tgtttccgcc 300
 acggaacgcc attaccgcat cagccagtgg gaatccagcg cctcatcgat agatgaatca 360
 ccagatgtga tttttgacta ctttatgctg gaaatgtctg acagccatga cgggctgttc 420
 ctcaacgccc agaagctgaa cgataaagcg attttgcctc gttctattaa ttcaccgctt 480
 tggatctgta cccttaaatac tggcagcaaa ttagac 516

<210> 121

<211> 546

<212> DNA

<213> Escherichia coli

<400> 121

atgaaaataa aagttatagc attggctaca tttgtttctg ctgtgtttgc tggttcagct 60
 atggcctatg acggaacaat tacgtttacc ggtaaagttg tagctcagac ctgcacagtt 120
 aatacaagcg acaaagactt agcagtaact ttaccactg ttgccacttc atctctaaaa 180
 gacaatgctg ctacgtcagg gctgacaccc tttgccattc gtttaactgg ttgtgcaact 240
 ggtatgaata gtgctcagaa tggttaaagcg tactttgagc cttcaagtaa cattgactta 300
 gctacacata atttaaaaaa tactgctact ccaactaaag cggataatgt acagattcag 360
 ttgctaaata gtaatggaac ttcaactatt cttttggggg aagcggataa tgggcaagat 420
 gtccagtctg agacaatcgg atctgatgga agtgccacat tgcgttatat ggcccagtat 480
 tatgcaacag gacaatctac cgcaggggat gtaaaagcga cgggtccatta taccattgcc 540
 tacgaa 546

<210> 122

<211> 1077

<212> DNA

<213> Escherichia coli

<400> 122

atgaaaagaa tctttttcat accattgttt ttaattttac tccctaagct ggcggtagcg 60
 ggtccggatg attatgtgcc ttcgcagata gcgggtaata catccacatt gccaggtggt 120
 gtgattggtc ctgctgatgc ccatacctat ccccggtgga taggagagct ggcgggaaca 180
 agtaaccagt atgtttttta tggcgggtgcc atcgtctctga tgcgtggaaa gtttacaccc 240
 gcactgccta aaattggaag tattacggta tactttccat caaggaaaca gcgtgattca 300
 tctgattttg atatctatga tattggtgta tccggactgg gtattattat tggcatggcg 360
 ggctattggc ccgcaacgcc tctgggtcccc ataaatagct caggtatata tattgaccct 420

gtaggtgcc aatacaaac caatacttat aacggtgcga cagcaagctt cggagctcgt 480
 ttgtttgttg cttttgtcgc aacgggaaga ttaccaatg gatataaac aatacccacc 540
 aggagcttg gtactatattt gttggaagca aaacgtacaa gtttaaataa taaaggactg 600
 acagcacctg ttatgttaaa tgggtgggcgc attcaggtac agagtcagac atgtaccatg 660
 gggcaaaaaa actatgtggt gccattaaat accgtatata aatcacagtt cacatctttg 720
 tataaagaaa tacaggagg taaaattgac atacacctac aatgcccgga tgggaattgat 780
 gtttatgcta cattgacaga tgcatacag ccagtgaaca gaacagatat attgacctta 840
 agcagtgaat ccactgcaaa aggatttggc atcaggctat ataaagacag tgatgtaact 900
 gccatcagct atggtgaaga ctcccctgtg aaaggaaatg gcagtcaatg gcactttctc 960
 gattacaggg gagaggtaaa tccacataac aatttaagag ccaattatat aaaaattgct 1020
 gatgcaacta cacctggaag tgtgaaggct attgcaacta ttactttctc atatcaa 1077

<210> 123

<211> 2532

<212> DNA

<213> Escherichia coli

<400> 123

atgaacgcta ataattctgtc atgcctgatt tactgtcgtt gttctcttct gctttttgct 60
 gcattagggg taacagtaac aaaccattca tttgctgctg aagaggctga gtttgattct 120
 gagtttttgc atttgataa agggataaat gctattgata tccgccgctt tagtcaggg 180
 aaccctgtgc ctgagggcag gtattattct gatatttatg ttaataatgt atggaagggg 240
 aaggctgatt tgcagtattt acgtactgcc aataccggtg ctccgacgtt atgcctgacg 300
 cctgagctgc tttcattgat tgatttagtc aaagatacta tgcgggaaa cacctcctgc 360
 tttccggcgt caacagggtt ttcttcagcc agaattaatt ttgacttata gactttaagg 420
 ttgaatatcg aaatccctca ggcactgctg aatacacgtc caagaggata tatttcccct 480
 gctcagtggc aaagtgggtg tcctgcagca ttataaaact atgatgctaa ctattaccag 540
 tatagctctt ccgggacgag taacgaacag acttatctgg gattaaaagc tggattcaat 600
 ttgtggggat gggctttgct ccaccgtggc agtgagagct ggaataatag ctatcctgcc 660
 ggatatcaga atatagaaac aagtataatg catgaccttg cccattgag agcacaattc 720
 acattagggg atttttatac gaatggtgag ctaatggata gcctcagttt gcggggagtc 780
 aggttagcat cggatgaacg aatgttacct ggctctttac gtggctatgc tcctgctgtc 840
 cggggaatag ctaacagtaa tgctaaagta accatttatc aaaatgctca taccctctat 900

gaaacgacgg tgccagccgg accatttgtc atcaatgatt tatatcccag tggatatgct	960
ggtgaccttc tcgttaagat aacagagtct aatggccaga cacgaatggt cacggttcct	1020
tttgccggccg ttgctcaact cattcgtccc ggatttagtc gctggcaaat gtcagtggga	1080
aagtatcggt atgcgaataa aacatataat gatttaatag cacaaggcac ctatcaatac	1140
ggcctgacga atgatattac tttaaacagt ggtcttacca cagcttcagg atatacagcg	1200
gggttagctg gcctggcctt taataccctt ctgggtgcta tagcatctga cattacattg	1260
tccagaacag cattcaggta ttccgggtgta acgcgtaaag gttatagtct gcaactcaagt	1320
tatagcatca atattccagc ctcaaacaca aatataactc tggcggctta tcgttattca	1380
tcaaaagatt tttatcatct gaaggatgcg ctatcagcta atcacaacgc gtttattgat	1440
gatgtttctg taaaaagtac agcgttttat cgtcccagga atcaattcca gatttcaatc	1500
aaccaggaat taggtgaaaa atgggggtggg atgtatttaa caggaacaac ctataattac	1560
tggggacata aaggaagtcg taatgaatac cagattgggt acagcaactt ctggaaacaa	1620
ctcggctatc aaattggatt gtctcagtc agagataatg agcaacaacg ccgtgatgac	1680
agattttata ttaattttac tctccctctg ggaggaagtg ttcaaagccc ggtgttttcc	1740
actgttttaa attatagcaa agaagagaaa aatagtattc agacatcaat tagtgggtact	1800
ggcggggagg ataatcagtt ctcttatggg atttcaggaa acagccagga aaacgggcct	1860
tccggttatg caatgaatgg gggttatcgt tcaocttatg taaatataac cacaacagtc	1920
gggcatgata ctcaataa taatcaaagg tcatttggtg cgtcgggagc ggtggtcgca	1980
caccctatg gagtgacatt gagtaatgac ctgagtgata cttttgccat tatccatgct	2040
gaaggagctc agggggctgt catcaataat gcctctggta gtctctgga tttttgggga	2100
aatgggtgtg ttccttatgt tacaccctat gagaaaaatc aaattagcat cgatccctcc	2160
aatttagatt tgaatgttga attatcggcg acggagcagg aaatcattcc tcgtgcta	2220
agcgccacgt tagtgaaatt tgacactaaa acaggaagaa gtctgttatt tgatattcgt	2280
atgtctactg gcaatcccc tccaatggct tctgaagttc tggatgaaca tggacagttg	2340
gccggatatg tcgctcaggc cgggaaggta tttaccaggg gactccctga aaaaggtc	2400
ctcagcgttg tatggggacc agataataaa gacagatgtt catttgtata tcatgttgca	2460
cacaataaag atgatatgca atctcagctc gttcctgttc tgtgtataca gcacccta	2520
caggaaaaaa ca	2532

<210> 124
 <211> 831
 <212> DNA
 <213> Escherichia coli
 <400> 124
 atgggtaaaat gtcatactct gattaaccgt agaaataaat gtctgtgat tgtttttata 60
 gtccttattg gatggattat attcagacct aaagcatata cttattcact aaatgataaa 120
 gaaaaagaga tgctcataat gttatcacia catcctgaaa ctcggtactt tggattttat 180
 tccatagaac ttcgggctga ttacaaacca acaggaatgg ttatgttcat acaaggatcg 240
 gcgatgatcc ctgtagaaac aaagctacaa tattatcctc cttttctgca atatatgaca 300
 cgatatgagg cagaactaaa aaacacctca gcattagatc cactggatac gccttatttg 360
 aagcaagttc acccactaag tccacctatg aatggagtca tttttgaacg aatgaaagcg 420
 aaatacacc cagatttttg acgagtattg gatgcatgga aatgggaaaa tggcgttacg 480
 ttttcagtaa aaatagaagc taaagatggg agagcaaccc gctatgatgg aattagtaag 540
 attgccgaat acagttatgg atataatatt ccagaaaaaa aagtacagtt acttactatt 600
 ctttcaggac tacaacctcg tgcagataac caacccccat cagaaaataa attggcgata 660
 caatatgcac aggttgacgc ttcactactt ggagagtatg aattatctgt agattataaa 720
 aatagcaata atattaaaat aagtttgcag acggataata atagttatat tgactcatta 780
 ttagatataa gatatccgag taatggaaac agagcatggg ataactctat a 831

<210> 125
 <211> 1098
 <212> DNA
 <213> Escherichia coli
 <400> 125
 atgctacctg agcctgttta tcgacgctgg attatattat taatatctat gttaacagtt 60
 ggtactctgt ttattttatc ggtctggaat tctgcgacat actgggatat ttttatttat 120
 ggcgttctgc caatgctgtt tctttggcta tgtttgtttg gtattgctgt gaacaaatat 180
 gaacaatccg ttgcagcctg tataagttgg gagtctgaaa gacaacaagt taaacaactc 240
 tggcaacact ggagccaaaa acaactggca atagttggga atgttctttt tacaccggaa 300
 gaaaaaggca tgagtgtttt actggggcca caggaagaga tccctgcata tccataaaaag 360
 gcacgacctg tattctctgc atcccgttat tctctttcgt ctatattcca tgatattcac 420
 cagcaactga cacaacaatt tcttgattat cgtcattatc tacatactat ctacgtatta 480
 cagcctgaga aatggcgtgg agaaaccgtg agacaggcta ttttccatca atgggactta 540

212

gtacctgaac ggaccaatac tcttaataca atccagtctc tttatgatga aagatttgac 600
 ggtctaattc tgggtggttg tttacaaaac tggccggaga ataaacctga agatacgagt 660
 gaactggtat cagcacagct tatctcctca tcgtcatttg tacggcagca ccagataccc 720
 gttattgctg gtctggggcg tgtaatgcca ttagaaccgc aggagttgga gcataatctg 780
 gatgtgttat ttgaatataa ccaattggat aacaaacaac tacagcatgt ctgggtctct 840
 ggttttagatg agggaaacgat agaaaacctt atgcagtatg ctgaacaaca tcaatgggtca 900
 cttcctaaaa aacggcccct acacatgatt gatcattcct ttggccctac aggagagttt 960
 atttttcctg tctctctggc aatgctgtca gaggctgcca aagaaactga acaaaatcat 1020
 ttaattatct atcagtcagc acagtatgct cagaaaaaga gcctttgcct gattaccgcg 1080
 aagctttatt taaggaca 1098

<210> 126

<211> 780

<212> DNA

<213> Escherichia coli

<400> 126

atgttgaaca gaaaactaaa tatacggcta cgtcattccc tgaacagtca ctgcatacct 60
 tccatcatta tcaataaacac cgtacgttca tttcagaggt cagtcatgaa taccagagct 120
 ctttttcccc tgctgttcac tgtggcatca ttctccgct ccgccggcaa ctgggctgtc 180
 aaaaacggct ggtgtcagac catgacggaa gatggtcagg cgttggtaat gctgaaaaat 240
 ggcacgattg gtattaccgg cctgatgcag ggatgcccga atggtgtaca gacgctcctg 300
 ggcagccgta tcagtattaa cggtaacctg atccccacat caaaaatgtg taatcagcag 360
 acgggattca gggctgttga ggtggaaatc ggacaggcgc cggaaatggt caaaaaagcc 420
 gttcactcca tagcagagcg tgatgtgtcc gttttacagg catttggtgt acgaatggaa 480
 ttcacccgcg gtgatatgct gaaggctctg ccgaaatttg tcacatcact tgccggtttt 540
 tccccgaaac agacgaccac tattaataaa gattccgtcc tgcaggctgc ccggcaggca 600
 tacgcccggg aatatgacga ggaaacaaca gaaaccgctg attttggtc ttacgaagta 660
 aaaggcaata aggttgagtt tgaagtattc aatcctgaag accgtgcgta cgacaaagtg 720
 accgtcacgg ttggtgctga cggtaatgcc accggcgcca gcgttgaatt tatcggaaaa 780

<210> 127

<211> 1155

<212> DNA

213

<213> Escherichia coli

<400> 127

```

gtggttaatta tcaatagcac gatactgagc ggcgagggcg ctatcccttc cctgacgtcg      60
ctcttaccog acatcagaaa aatgctgctg gtcactgacc gtaatatgtc gcagctcgac      120
gggtgtgcagc agattcgcgc cttactggaa aagcactgcc cgcaggttaa cgttatcgat      180
aatgtgcccg cagagcccac gcatcatgat gtgcgccagc taatggatgc ccctggcgat      240
gcctcttttg atgtgggtgt cgggatcggc ggtggcagcg tggtggatgt ggcgaagctg      300
ctatcggtgc tttgccatcc acaatcaccg gggctggatg cgctgcttgc gggtgaaaaa      360
ccgactcagc gggtgcaatc atggttgatt cctacaaccg ccggaaccgg ctcagaagcc      420
acgccgaatg cgattctggc aatccctgag caaagcacga aggtgggtat tatttcccag      480
gtgctgttac cagactatgt ggcgcttttc ccggaactga ccaccagcat gcccgcgcac      540
attgcggcgt ccacgggcat tgatgctctt tgccacttac tggagtgttt taccgcgacc      600
gtggcaaate cggtcagcga taacgcggcg ctgactgggt taagtaaact tttccggcac      660
attcaaccgg ccgtgaacga toctcaggat ctgcgcgcaa aactggaaat gctgtgggcg      720
tcttactatg gcggcgtagc gataacccat gcgggcacgc atctcgttca tgcgctctcc      780
taccggttag gtggcaaata tcatctgccg catggcgctc cgaatgccat cttgctggcg      840
ccgtgcatgg cgtttgttcg cccctgggcg gtcgagaaat ttgcccggtt ctgggattgc      900
attcccgatg cggaaaccgc cctgagcgcg gaagaaaaat ctcatgccct ggtgacctgg      960
ttacaggcat tagtcaatca actcaagcta cccaacaate tcgcggtctc cggcgctaccg     1020
ccagaggata ttgcctctct gagcgaggcg gcaactgaac tgaagcgctt tatgaacaat     1080
gtgcggtgcc aaattgatct acaggacgta caggccattt accaaacact gtttccgcaa     1140
catccattta aggag                                           1155

```

<210> 128

<211> 315

<212> DNA

<213> Escherichia coli

<400> 128

```

atgaatatca gaaaactgtt ttgtccggga aacacccccc ggattttatt gtttttatcc      60
ttttttgttg tttctgcaat aaccacaatt gcatgaggat aactgagaa gaatgcaaca      120
ggaaatgtgc tgcttctgtt tctccttctg ctcttgcac acagaaatac cctcacatcc      180
attacagcgc tgttatttct gttctgttgt gcaactgtat gcctgcccgg tatgacgtac      240
ggtaaaatca acaacagttt tattgtgcg ttgttgacga ccacaactga tgaggcagcg      300

```

gagttttaccg ggatg

315

<210> 129

<211> 441

<212> DNA

<213> Escherichia coli

<400> 129

atgaatatc aggcaataaa agaaatggta aatttaattt gtagtttttt atttatatc 60
 tttctgtcct cggcttttgt ttcttttggg tggtatgcta tttatgaatt gtttttatgg 120
 aatgatatta ttgtatatag ctggggatat atattaattg tctttttacc tttcacatta 180
 tatgtaatgt cgtttgagat tttgtttttt gctattagtg ggcgacgatt gtctaaagta 240
 acaatgggtgc gcctttgggt gataattaaa attattattg ctttctctat ttgcgcagtg 300
 ttgatttttt cttcaattta caaaaaagaa ttattatcta gaaattatat tgctttagtg 360
 ggtatcccggt ctgggtggat gccgggtctg gcaacgaaat acgttaaaga aaaatcatta 420
 tgcgaaaaaa atggcaataa t 441

<210> 130

<211> 534

<212> DNA

<213> Escherichia coli

<400> 130

atgttttcta ttcgttttaa acgtccggcg ttgctctgta tggcgatgct gacggttggt 60
 ctgagtggct gcgggctgat tcagaaagtg gtggatgaat cgaaaagcgt ggcctcagcc 120
 gttttctaca aacaaatcaa aatactgcat ctcgatttct tctcccgag cgccctgaat 180
 acggatgcgg aagatacgcc gctttccacg atgggtgcatg tctggcaact gaaaaccgcg 240
 gaagattttg acaaggcgga ttacgacacc ctgtttatgc aggaagagaa gacgctggag 300
 aaggacgtac tggcaaaaca caccgtctgg gtaaaaccgg aaggcacggc atccctgaat 360
 gtgccgctgg ataaagagac gcagtttgct gccattattg ggcagtttta tcaccctgat 420
 gaaaaaagcg acagctggcg tctggtgatc aaaagggacg aactggaggo cgacaagccg 480
 cgctcgattg aactgatgag aagcgacctg cgactgctgc ctctcaagga taaa 534

<210> 131

<211> 627

<212> DNA

<213> Escherichia coli

<400> 131

atgttcttaa aaagaaaatg gtattacgca gtgacgacat ctgtcgtcat tactttgtgt 60

ggtggaggat attatatgta caggcaagaa tatcagatgg ttgtcactgt accaactgct 120
 gacgcgaacg atcccaactg gccaaataaa aggatacagt ttgataccag cgaatggcta 180
 cagcaacttc aatatattaa aatagatgat cattatatat tgaatactca atatactcca 240
 attgctaatt tggatgactt tggattaca ttaaaattac agaacgcatt aaatgggtcg 300
 gataaaagac ttcctgcact atatggcctt gctgagatgg atgctcagaa atttaaagac 360
 ctgatgcgcg gtaaaattaa atgtgaatat ctgaggacga catttgatgc ggaaacatta 420
 aagcctgtca atgattatct ccttatttct tttacttata aagataagt gtatgaattt 480
 gagacagaaa gaaaaatatc taaaacaagt gatgatgggt attttttctg ggcatttgat 540
 aatactgtcc acgaagcagg ctattggcat aacacagatc cggctgcgta ttcctataga 600
 gattaccaga atggtaaggc tgtgaaa 627

<210> 132

<211> 1272

<212> DNA

<213> Escherichia coli

<400> 132

atggatatctt ggcggggaca ttcgtttctg atgacaattt ccgctagggt cagacaatac 60
 gttttctctc ttatgtcaat ttattgcag gaacgaaaaa tgaatatctt cactttatcc 120
 aaagcaccgc tatacctgtt aatttcacta tttttaccca cgatggccat ggctatcgat 180
 ccacctgaac gcgaacttct gcgatttgcc ctgaaaacga attaccttca gtcccctgat 240
 gaaggcgtct atgaactggc gtttgataat gccagtaaaa aggtgtttgc agcagtcacc 300
 gatcgtgtaa atcgtgaagc caataaaggc tatctgtatt cgtttaattc agattcgctg 360
 aaagtcgaaa ataaatacac gatgccatac cgggcatttt cgctggcgat aaatcaggat 420
 aaacatcagc tctatatcgg acacacccag tcagcgtccc tgcgtatcag tatgtttgac 480
 accccaaccg gcaaactggg aagaaccagc gacagggtta gttttaaagc ggcaaacgct 540
 gcagattcgc gttttgagca ttttcgccat atggtttaca gccaggattc cgataccctg 600
 tttgtgagtt atagcaatat gctgaaaacg gccgagggca tgaagcctct gcataagctg 660
 ttaatgctcg acgggacgac gcttgcccta aaaggcgagg ttaaggatgc ttacaaaggc 720
 acagcgtatg gtctgacgat ggatgaaaaa acacagaaaa tctacgttgg cggaagagat 780
 tacatcaacg aaattgatgc gaaaaatcag acgctgctgc gtaccatccc gttgaaagat 840
 ccgagaccac aaatcacaag tgtgcagaat ctggcggtgg actccgcttc tgaccgtgcc 900
 tttgtggtgg tattogacca tgacgatcgt tccggtacaa aagatggact ctatatcttt 960

Seq ID 133

MAIPAYLWLKDDGGADIKGSVDVQGREGSIEVVALDHDVYIPTDNNTGKL
TGTRTHKPFTFTKEIDASSPYLYKAVTTGQTLKTAEFKFYRINDAGQEVE
YFNITLDNVKLVRVAPLMHDIKDPREKHNHLERIEFRYEKITWTYKDG
NIIHSDSWNERPSA

Seq ID 134

VRNTLKQAIVLWGMVLLLVLWSVFISSPGVLRWAGAAIIVLAVAALLIYR
RRQAWTEMTGDAGLSSLPPEYRQPVVLVCGGLSAHLSTDSPVRQVSEGL
YLHVPDEEQLVAQVERLLTLRPAWASQLAVAYTIMPGIHRDVAVLGRRLR
RFAHSMATVRRRAGVNV PWLLWSGLSGSPLPERASSPWFICTGGEVQVAT
STETTPAQWIAQSGVQERSQRLCYLLKAESLMQWLNLNVLTAALNGPEAK
CPPLAMTVGLVPSLPAVDNNLWQLWITARTGLTPDIADTGTDDALPFPDA
LLRQLPRQSGFTPLRRACVTMLGVTTVAGIAALCLSATANRQLLRQVGDD
LHRFYAVPVEEFITKARHLSVLKDDATMLDGYREGEPLRLGLGLYPGER
IRQPVLRRAIRDWRPPEQKMEVTASLQVQTVRLDSMSLFDVGQARLKDGST
KVLVDALVNIRAKPGWLIIVAGYTDATGDEKSNQQLSLRRAEAVRNWMLQ
TSDIPATCFVQGLGESQPAATNDTPQGRAVNRRVEISLVPRSDACQDVK

Seq ID 135

MIKSTFWRALALTATLILTGCSHSQPEQEGRPQAWLQPGTLITLPAPGIS
PAVNSQQLTGSGFNGKTQSLVLMNAEDQKITLAGLSSVGIRLFLVTYDA
KGLRAEQSIVVPQLPPASQVLADVMLSHWPI SAWQPQLPTGWLTRDNGDK
RELNRNASGKLVTEITYLNRQGRVPISIEQHVFKYHITIQLYLD

Seq ID 136

MKRYIKWFAITIFISMLSACVRTAPVQQISTTVSVGHTQEQVKNAILKAG
AQRKWIMTQVSPGVIKARYQTRNHVAEVRITYTATYYNIKYDSSLNLQAS
DGKIHKNYNRWVRNLDKDIQVNLSTGATL

Seq ID 137

MKRKHLLLLLLFSFSTNSAPLYSLIREAVMHDPIVMEARAELTSAQSRIE
QASSAHWPVVTATGSKLLSQSHRYSYDYDTEDILPGIRGEVNI FASGAIE
ADVRRSESEAEYYHYKMEETKEETIHSFVSLYLDALREKQSI AVLEQSL
RHNAIILNDLNTISIHDTGRESELVQAEARRLMVRQQINRSRVLKTTLGK
LSTWTKNPVTEADLENPF SRMTEAKLLTDFTQAPQKGNPSWLASQADVES
KKAALKAQELARYPRVDLTGSVTRDDQQIGVNLSDWLFNRNASYGVTEKA
AQIVAATGRLD SVARMIDETGRLSLITVRQSRGEMETLRRQEQASARVVD
FYRLQFQVARKTLIELLNAENELYSVGLSRVQTEDQMLHGMLDYLYSQGM
LLKWSGVNLSGEEK

Seq ID 138

MKFLPLLALLISPFVSALTLDLQQRFTQEPVIRAHFDQTRTIKDLPOPL
RSQGQMLIARDQGLLWDQTS PFPMQLLLDDKRMVQVINGQPPQIITAENN
PQMFQFNHLLRALFQADRKVLEQNFRVEFADKGEGRWTLRLTPTTTPLDK
IFNTIDLAKGTYLESIQLNDKQGDRTDIALTQHQLTPAQLTDDEHQRF
AAQ

Seq ID 139

MENFFMKNSKVFYRSALATAIVMALSAPAFATDSTVSTDPVTLN
TEKTTLDQDVVINGDNKITAVTIETSDSDKDLNVTFGGHDITAASTVNQD
FVEGVKVSNGKNV VINATDSTITAQEGTYVRTAMVIDSTGDVVVNGGNF
VAKNEKGSATGISLEATTGNLTLNGTTINAQGNKSYNGSTAI FAQKGN
LLQGFQGDATDNITLADSNIINGGIETIVTAGNKTGIHTVNLNIKDSVI
GAANNKQTIYASASAQAGSATQNLNLSVADSTIYSDVLALSESENSAST
TTNVNMNVARSYWEGNAYTFNSGDKAGSDLDINLSDSVWKGKVSAGDA
SVSLQNGSVWNVTGSSTVDALAVKDSVTNITKATVNTGTFASQNGTLIVD
ASSENTLDISGKASGDLRVYSAGSLDLINEQTAFISTGKDSTLKATGTTE
GGLYQYDLTQGADGNFYFVKNTKASNASSVIQAMAAAPANVANLQADTL

SARQDAVRLSENDKGGVWIIQYFGGKQKHTTAGNASYDLVDVNGVMLGGDTR
FMTEDGSLAGVAMSSAKGDMTTMQSKGDEGYSFHAYLSRQYNNIGIFID
TAAQFGHYSNTADVRLMNGGGTIKADFNTNGFGAMVKGGYTWKDGNGLFI
QPYAKLSALTLEGVDYQLNGVDVHSDSYNSVLGEAGTRVG YDFAVGNATV
KPYLNLAAALNEFSDGNKVR LGDES VNASIDGAAFRVGAGVQADITKNMGA
YASLDYTKGDDIENPLQGVVGINVTW

Seq ID 140

MSRPQFTSLRSLALLAVSATLPTFAFATETMTVTATGNARSSFEAPMMV
SVIDTSAPENQTATSATDLLRHVPGITLDGTGR TNGQDVNMRGYDHRGVL
VLVDGVRQGTDTGHLNGTFLDPALIKRVEIVRGPSALLYGSGALGGVISY
DTVDAKDLLQEGQSSGFRVFGTGGTGDHSLGLGASAFGR TENLDGIVAWS
SRDRGDLRQSNGETAPNDESINNMLAKGTWQIDSAQSLSGLVRYNN DAR
EPKNPQTVEASDSSNPMVDRSTIQRDAQLSYKLAPQGN DWNADAKIYWS
EVRINAQNTGSSGEYREQITKGARLENRSTLFADSFASHLLTYGGEYYRQ
EQHPGGATTGFPQAKIDFSSGWLQDEITLRDLPITLLGGTRYDSYRGSSD
GYKDVDADKWSSRAGMTINPTNWLMLFGSYAQAFRAPTMGEMYNDSKHFS
IGRFYTNYPNP NLPETNETQEYGFGLRFDDLMLSNDALFKASYFDT
KAKDYISTTVDFAAATTMSYNVPNAKIWGWDVMTKYTTDLFSLDVAYNRT
RGKDTDTGEYISSINPDTVTSTLNIPIAHSGFSVGWVGTFADRSTHISS
YSKQPGYGVNDFYVS YQGQALKGMTTTLVLGNAFDKEYWSPQGI PQDGR
NGKIFVSYQW

Seq ID 141

MRDEMLYNIPCRIYILSTLSLCISGIVSTATATSSSETKISNEETLVVTTNRSASN LWESPATIQVIDQQT LQNSTNASIA
DNLQDIPGVEITDNL LAGRKQIRIRGEASSRVLILIDGQEVTYQ RAGDNYGVGLLIDESALERVEVVKGPYSVLYGSQAI
GGIVNFITKKGDKLASGVVKAVYNSATAGWEESI AVQGSIGGF DYRINGSYSDQGNRDTPDGRLPNTNYRNNSQGVWLG
YNSGNHRFGLSLDRYRLATQTY YEDPDGSEYAFSVKIPKLEREKVG VFYD TDVDGDY LKKIHF DAYEQT IQRQFANEVKT
TQPVPSPMIQALT VHNKTDTHDKQYTQAVTLQSHFSLPANNELVTGAQYKQDRVSQRSGGMTSSKSLTG FINKETRTRSY
YESEQSTVSLFAQNDWR FADHWTWTMGVRQYWLSSKLTRGDGVSYTAGIISDTSLARESASDH EMTSTSLRYSGFDNLE
LRAAFAQGYVFPTLSQLFMQTSAGGSVTYGNPDLKAHSNNFELGARYNGNTWLIDS AVYYSEAKDYIASL ICDGSIVCN
GNTNSSRSSYYYDNIDRAKTWGLEISAEYNGWVFSPYISGNLIR RQYETSTLKTNTTGEPAINGRIGLKHTLVMGQANI
ISDVFIRAASSAKDSSNGTETNVPGWATLNF AVNTEFGNEDQSRINLALNNLTDKRYRTAHETIPAAGFNAAIGFVWNF

Seq ID 142

MRKVCVILSAAICLSVSGAPAWASEHQSTLSAGYLHARTNAPGSDNLNGINVKYRYEFTDALGLITSFSYANA EDEQKT
HYS DTRWHEDSVRNRFVSMAGPSVRVNEWFSAYSMAGVAYS RVSTFSGDYLRVTDNKGKTHDVL TGSDDGRHSNTSLAW
GAGVQFNPTESVTIDLAYEGSGSGDWRTDAFIVGIGYRF

Seq ID 143

MKKSTLSLAIGLLACSTGMAKTQHLTLEQRLEAAEMRAAKAEGQVKQLQ
TQQA AEIREIKTAQGNTPVNGQSTTESEKKNATPPNLLLSGYGDLKIYGD
VEFNMDAESNHGLLAMTNADVNSDPTNEWNLNGRILLGFDGM RKL DNGY
FAGFSAQPLGDMHGSVNIDDAVFFF GKENDWKVKVG
RFEAYDMFPLNQDTFVEHSGNTANDLYDDGSGYIYMMKEGRGRSNAGGNF
LVSKQLDNWYFELNTLLEDGTSLYNDGNYHGRDMEQQKNVAYLRPVI AWS
PTEEFTVSAAMEANVVNNAYGYTDSKGNFVDQSDRTGYGMSMTWNLKTD
PENGIVVNLNTAYLDANNEKDFTAGINALWKR FELGYIYAHNKID EFGSV
VCDNDCWIDDEGTYN IHTIHASYQFANVMDMENFNIYLGTYYSILDS DGD
KIHGDDSDDRYGARVRFKYFF

Seq ID 144

MNGKAFLACVLMSVVL TGCETAKKISQVIRNPDIQVGKLM DQSTELTVTLLTEPD SNLTA
DGEAAPVDVQLVYLSDDSKFHAADYDQVATTALPDVLGKNYIDHQDFNLLPDTVKTL PPI
KLDEKTGYIGVIAYFSDDQATEWKQIESVESIGHHYRLLVHIRASAIEMKKEEN

Seq ID 145

LT LAWIFLLVWIWQGP KWTLYEQHWLAPLANRWLATAVWGLIALVWL TWRVMKRLQKLEKQQKQOREEEKDPLTVELHR
QQQYLDHWLLRLRRHLDNRRLWQLPWYMVIGPAGSGKSTLLREGFP SDIVYTPESIRGVEYHPLITPRVGNQAVIFDVD

GVLTPPGDDLLRRRLREHWLGWLMQTRARQPLNGLILTLDPDLLTADKSRRETLVQNLRRQLQEIQRSLHCRLPVYVV
LTRLDLLNGFAALFHS�DKDRDAILGVTFTRRAHESDGRSELGAFWQTWVQVNLALSDLVLAQTGAAPRSVFSFSR
QMGGTGEIVTALLAALLDGENMDVMLRGVWLTSLSLQRGQVDDIFTQSAARQYGLGNSSLATWPLVETTPYFTRRLFPEVL
LAEPNLAGENSVDLNSRRRLTAFSTCGAALAALMVGSWHYNNQNWQSGVNVLAQAKAFMDVPPQGTDEFGNLQPLL
NPVRDATLAYGDYRDHGFADMGLYQGARVGPYVEQTYIQLLEQRYLPSLMNGLIRDLNIAPPESEEKLAVLVRVMMED
KSGRNNEAVKQYMARRWSNEFHGQORDIQAQLMVHLDYALEHTDWAHQRSSSDSDAVSRWTPYDKPIINAQQELSKLPYQ
RVYQTLRTKALSVLPAIDLNLRDQVGPTFDNVFVAGNDEKLVIPOFLTRYGLQSYFVKQREGLVELTALDSWVLNLTQSV
YSEADREEIQRHITEQYISDYTATWRAGMDNLNVRDYEAMSALEEQDKASTLQAVYQQLTELHRYLLAIQNSPVPKSAKAVQLRLDQNSSDP
IFATROMAKTLPAPLNRWVGKLADQAWHVVMVEAVRYMEVDWRDNVVKPFNEQLADNYPFNPRATQDASLDSFERFFKPD
GILDNFYKNNLRLFLENDLTFGDDGRVLIREDIRQQLDTAQKIRDIFFSQQNGLGAQFAVETVSLSGNKRRSVLNLDGQL
VDYSQGRNYTAHLVWPNNMREGNESKLTIGTSGRAPRSIAFSGPWAQFRLFGAGQLTNVTSDTFNVRFNVDGGAMVYQV
HVDTEDNPFTGGFLSFLRPLDPLY

Seq ID 146

ATGGCTATTCTGCTTATCTCTGGCTGAAAGATGACGGCGCGCGGATATCAAAGGTTCCGTGGACGTTACAGGGCGCGA
AGGTAGCATCGAAGTGGTGGCGCTGGATCAGATGTGTACATCCCGACCGACAATAACACCGGCAAACTGACCGGTACCC
GTACTCACAAGCCTTTTACGTTTACCAAAGAAATCGATGCGTCCAGCCCGTATCTCTACAAAGCTGTGACCACCGGACAG
ACCCTGAAAACGGCAGAATTTAAGTTTTACCGCATCAACGATGCCGGTCAGGAAGTGGAGTACTTCAACATCACGCTTGA
TAACGTCAAGCTGGTCAGAGTCGCTCCGCTTATGCACGACATCAAGGATCCTTCCAGAGAGAAGCATAACCACCTGGAAC
GTATTGAGTTCCGCTACGAGAAAATCACCTGGACTTACAAAGACGGCAACATCATTATTCCGACTCGTGGAATGAGCGT
CCTTCCGCC

Seq ID 147

GTGAGGAACACGTGAAACAGGCCATCGTGCTGTGGGAATGGTGTACTGCTGGTGTGTGGTCACTGTTTATCAGTCC
GTCTGGCGTGTGAGATGGGCCGGTGCGGCGCTATCGTTCTGGCGGTTGCCCGGTTGTTGATTTATCGGCGCAGGCAGG
CGTGGACGGAGATGACCGGCGATGCCGGGTTGTCATCGCTGCCGCCGGAACCTACCGACAGCCGGTAGTGCTGGTCTGT
GGCGGTCTGTGGCGCACCTGTCCACTGACAGCCCGGTCCGCCAGGTTTTCAGAAAGGCTGTATCTGCATGTTCTCTGATGA
AGAACAGCTTGTGGCGCAGGTGGAGCGATTGCTGACCCTTCGCCCCGGCTGGGCATCGCAGCTTGGCGTGGCGTATACCA
TCATGCCCCGCATACACCGGGATGTGGCGGTTCTGGCCGGACGGCTGCGACGCTTCGCCCACAGTATGGCGACGGTGCGT
CGTCGGGCAGGCGTAAACGTCCCCTGGCTTCTCTGGAGCGGGCTGTCCGGCTCGCCGTTCGCGGAAAGAGCGAGTTTACC
GTGGTTTATCTGTACCGGCGGCGAAGTTTACGGTAGCAACATCCACAGAGACCACCATGCCCGCGCAGTGGATTGCACAAT
CCGGCGTACAGGAGCGCAGTCAGCGACTCTGTTACCTGCTGAAAGCTGAAAGCCTGATGCAGTGGCTGAATCTTAATGTG
CTGACGGCACTGAACCGGCCGGAGGCGAAATGTCCACCCTGGCGATGACCGTGGGGCTGGTCCCTCGTTGCTGCTGGT
GGATAACAACCTGTGGCAGTTGTGGATCACCCCGAGAACCAGGCTGACGCCGATATCGCGGACACCGGCACAGCAGTG
CGCTGCCATTCCCGGATGCCCTGTTACGGCAGTTGCGCGCTCAGTCGGGCTTTACCCCGCTGCGACGAGCCTGCGTGACC
ATGCTGGGCGTACCACCGTGGCGGGTATCGCCGCGCTGTGCTGTGAGCCACGGCAAATCGCCAGTTATTACGGCAGGT
CGGTGACGATCTGCACCGGTTTTATGCCGTCCCGGTGGAGGAATTTATACCAAAGCCCGTCACCTGTGGTGTGAAAG
ACGATGCGACCATGCTCGATGGGTATTACCGGGAAGGAGAACCCTGCGCCTCGGTCTGGGGTTATACCCCGGCGAACGC
ATCCCGCCAGCCGTTATTACGCGCCATTGCGGACTGGCGTCCGCTGAAACAAAAAATGGAGGTGACGGCTTCGCTTCAGGT
TCAGACCGTGGTCTTGACAGTATGTGCTGTTGACGTCGGACAGGCCCGCTGAAAGACGGCTCGACAAAAGTGCTGG
TGGACGCACTGGTGAACATCCGGGCAAAACCGGGCTGGCTGATCCTCGTGGCCGGATATACCGATGCCACCGGCGATGAA
AAAAGCAATCAGCAGTTATCGCTGCGGCGTGCCGAAGCGGTGCGCAACTGGATGCTGCAGACCAGCGACATCCCGGCCAC
CTGTTTTGCGGTACAGGGACTGGGCGAGAGCCAGCCTGCGGCGACCAACGACACGCCACAGGGCCGGGCGAGTCAACCGGC
GTGTCGAAATCAGTCTTGTTCCGCGTTCTGACGCTGTGACGAGCTGAAA

Seq ID 148

ATGATCAAATCCACATTCTGGCGAGCGCTCGCCCTGACCGCTACGCTTATCCTCACTGGCTGTAGCCACTCGCAACCGGA
ACAGGAAGGCCCGCCGAGGCGTGGCTGCAACCTGGTACGCTCATCACGCTGCCTGCGCCGGGGATTTACCCGCGAGTCA
ATTCCCAGCAACTGTTGACCGGCGAGCTTCAACGGCAAAACCCAGTCTCTGCTAGTGATGCTTAATGCCGAAGATCAGAAA
ATCACCTTCCCGGCTGCTCGTGGTCCGCTGCGCTGTTTCTGGTGACCTACGATGCAAAAGGGCTACGCGCCGAGCA
ATCCATCGTGGTCCGAGTATCCGCCCGCAAGTCAGTACTGGCTGACGTGATGCTCAGCCACTGGCCGATTAGCGCCT
GGCAACCGCAACTTCCACAGGCTGGACGCTTCCGACAGCAGCGGACAAACGAGCTGCGTAACGCCAGCGGCAAACTG
GTCACGGAAATCACCTATCTGAATCGCCAGGGAAAACGCGTGCCAATCAGCATTGAGCAGCATGTCTTTAAATACCACAT
CACCATTCAATACTTAGGTGAC

Seq ID 149

ATGAAACGTTATATAAAATGGTTTGGCCATCACAATTTTTATCAGTATGTTGAGTGCCTGTGTCCGTACGGCCCCAGTGCA
ACAGATAAGCACCAGTGTCTAGTGTGGGTCTACTCAGGAGCAGGTTAAAAATGCCATTTTGAAGCAGGTGCGCAGCGCA
AGTGGATTATGACGCAAGTGTCCCCTGGAGTTATTAAAGCTCGCTATCAAACACGAAATCACGTTGCAGAGGTTCTGTATT
ACATATACAGCTACCTACTATAACATCAAATATGACAGTAGCCTGAATCTGCAGGCTTCTGTATGGAAAAATTCATAAAAA
CTATAACCGCTGGGTGCGTAACCTGGATAAAGATATACAGGTTAACTTATCTACAGGAGCAACGTTA

Seq ID 150

ATGAAGCGTAAACATTTGTTATTATTATTGTTGTTTTTCATTTTCCACTAACAGTGCCTCTTTACTCCTTAATTAGGGA
GGCAGTTATGCACGATCCCATAGTAATGGAAGCCCGGGCGGAGTTAACTTCGGCACAATCCCGCATAGAGCAGGCAAGCT
CTGCACATTTGGCCAGTTGTACAGCTACAGGAAGTAAACTCCTTTACAAAGTCACCGTTATTCTACGATTATGACACT
GAAGATATTTTACCCGGTATTCGTGGTGAAGTGAATATATTTGCTTCAGGGGCTATTGAGGCGGATGTGCGTGGAGTGA
GTCAGAAGCCGAATATTATCATTATAAAATGGAAGAAACAAAAGAGGAAACAATTCACTCTTTTGTTCATTATATCTTG
ATGCACTCAGGGAACAAATCCATTGCGGTACTTGAACAGAGCCTTTCCCGGCATAACGCAATTCTTAATGACCTGAAT
ACCATCAGTATTCATGATACCGGGCGGGAGTCTGAGCTTGTTTCAGGCCGAAGCCAGAAGGTTGATGGTTCCGCGACGAT
AAATTCCTAGGAGCAGAGTACTTAAACCACGCTGGGAAAACCTGTCCACTTGGACAAAAAATCCGGTAACCGAAGCTGATC
TTGAAAACTCTTTTCTAGGATGACAGAGGCCAAATTAATTAAGTATTTTACACAGGCTCCACAGAAAGGTAACCCGTCG
TGGCTTGGCAGCCAAGCTGATGTTGAGAGTAAAAAAGCGGCACTGAAAGCACAGGAGCTTGCCCCGTACCCCTCGGGTGG
TTAAGCGGGTCTGTAACCCGGGATGACAGCAGATAGGGGTCAATCTGTCTTGGGACCTCTTTAACCGTAATGCCAGTT
ATGCTGTTTACGAAAAAGCTGCGCAAATAGTGGCAGCTACCGGACGACTGGAGCTGTGTCGCCCGAATGATTGATGAAACC
GGGCGATTATCTCTGATAACAGTCAGACAAAGTCGAGGGGAAATGGAACGCTCAGACGTCAGGAACAGGCTTCAGCCAG
AGTTGTGGACTTTTATCGTCTTCAGTTTCAGGTGGCAAGAAAAACACTGATTGAATTACTGAATGCTGAAAACGAACTGT
ACAGTGTGCGACTCTCCCGGGTTTCAGACGGAGGATCAGATGCTCCACGGTATGCTGGATTATCTGTATTCCCAGGGAATG
CTCTGAAATGGAGCGGAGTGAATCTTTCTGGTGAAGAAGAAAA

Seq ID 151

ATGAAATTTTTACCGCTGCTGGCGCTGCTGATTAGCCCGTTTGTGAGCGCCCTGACCCTGGACGATCTTCAGCAACGCTT
TACCGAACAAACCGGTGATCCGCGCCCATTGATCAAACCCGGACGATTAAAGATCTGCCGACGCCGCTGCGATCTCAGG
GTCAGATGTTGATCGCCCGGACACCGGGGTATTGTGGGATCAAACCTCACCGTTCCTCCATGACGATATTGCTGGATGAT
AAACGCGATGGTGCAAGTGAACAGGTCAACGGTCAGCCGCGCAAATCATCAGCGCAGAAAAACAACCCGAGATGTTCCAGTTAA
CCACCTGCTGCGCGCGCTGTTCCAGGCCGATCGCAAAGTGCTGGAACAAAACCTTCGCGCTCGAATTTGCTGCAAAAGCGC
AAGGCCGCTGGACGCTGCGCCTGACGCCGACCACCGCCGCTGGATAAAATTTTCAACACCATCGATCTCGCCGGGAAA
ACCTATCTGGAGAGCATTCAACTTAATGATAAACAGGGCGATCGCACCGATATTGCTCTTACCCAACATCAACTGACGCC
AGCGCAACTGACCGATGACGAACACCAACGTTTTGCGGCCAG

Seq ID 152

ATGAAAAACAGTAAGGTATTTTACCGCAGCGCATTAGCGACAGCTATTGTTATGGCTCTTTCTGCACCAGCATTGCTAC
TGATAGCACGGTATCAACTGATCCGGTTACGCTGAATACAGAGAAGACGACTCTGGATCAAGATGTTGTTATTAACGGTG
ATAACAAGATTACAGCCGTAACAATTGAAACGTCAGATTTCAGATAAAGACCTTAATGTTACTTTTGGCGGTCACGATATT
ACCGCCGATCAACCGGTAAACCAAGATTTTCGTTGAAGTTGATAAAGTTAGTGGTAACAAAAATGTTGTGATTAATGCTAC
AGACTCCACCATCACAGCTCAAGGTGAAGGCACCTATGTCCGACTGCAATGGTCATTGATTCAACTGGCGATGTTGTTG
TTAATGGCGGTAATTTTCGTTGAAAAATGAAAAAGGTAGTGCGACAGGGATATCTCTGGAAGCGACGACCAGGGAATAAT
TTAACGCTCAATGGTACAACCATAAATGCTCAAGGTAATAAGAGTTACAGCAACGGCTCTACGGCAATTTTTGCTCAAAA
GGGTAATTTGTTGACGGGTTTTGACGGTGTGCAACCGACAACATCACCTTGCTGACTCAAATATTATTAATGGCGGGA
TTGAAACAATAGTTACTGCCGGGAATAAGACGGGAATTCATACAGTCAACCTGAATATTAAGGATGGCTCAGTAATTGGG
GCGGCTAATAATAACAACAATTTATGCCTCTGCTTCGGCACAAGGCGCAGGTTACAGCAACGCAAAATTTAAATTTGTC
TGTTGCTGATTCAACCATCTACTCTGATGTCTTGGCCCTTTCTGAAAGCGAGAATTCAGCCAGTACCACAACAATGTAA
ATATGAACGTTGCCCGCTCTTACTGGGAAGGTAATGCTTATACCTTCAATAGCGGCGATAAAGCGGGTAGTGATCTGGAT
ATAAATCTTTCCGATAGTTTCAGTCTGGAAAGGCAAGTTTCAGGGGCGAGGATGCCAGTGTATCTCTGCAAAACGGGTC
TGTCTGGAATGTTACGGGTTCTCAACTGTTGATGCTCTGGCAGTAAAGACAGTACGGTTAATATCAGGAAGGCTACAG
TCAATACTGGCACGTTTGTCTCTCAAAACGGCACTCTGATTGTTGATGCCTCTTCTGAAAAACACTCTGGATATCAGCGGT
AAAGCGAGCGGTGACTTGCCTGTTTACAGTGCAGGTTTCATTGGATCTTATCAATGAACAAACGGCATTTATTTCTACCGG
CAAAGACAGCACTCTAAAAGCCACAGGCACAACGGAAGGTGGTCTGTATCAATATGACCTGACACAGGGAGCTGATGGTA
ACTTTTATTTTCGTAAAAACACGCATAAAGCATCCAACGCCAGCTCCGTGATTACAGGCAATGGCAGCTGCTCCGGCTAAC
GTCGCTAATCTGCAGGCTGACACGCTCTCCGCCCGTCAGGATGCTGTCCGTCTGAGCGAAAATGACAAGGGTGGCGTATG
GATTACGTAATTTGGCGGTAAACAGAAACATACCACCGCGGGAATGCATCCTATGACCTGGATGTAAATGGTGTAAATGC
TGGGTGGTGATACCCGCTTCATGACTGAAGATGGTAGCTGGCTGGCCGGTGTGGCGATGTCTTCTGCGAAAGGTGACATG
ACTACCATGCAGAGCAAAGGTGACACTGAAGGTTACAGCTTCACGCTTACCTGAGCCGCCAGTATAACAACGGTATCTT
CATTGATACTGCTGCAAGTTTGGTCACTACAGCAACACGGCAGATGTTTCGCTGATGAATGGTGGCGGTACCATCAAAG
CTGACTTTAACACCAATGGTTTTTGGTGGCGATGGTTAAAGGCGGTTACACATGGAAGACGGTAATGGCTGTTTTATTACG

CCATATGCCAAACTGTCTGCTCTGACTCTGGAAGGTGTGGATTATCAACTCAACGGCGTGGACGTTTCATTCTGACAGCTA
TAACTCTGTGCTGGGTGAGGCCGGTACGCGCGTGGGTATGACTTCGCTGTGGGCAACGCGACCGTTAAACCTTATCTGA
ATCTGGCCGCACTGAACGAATTCTCTGATGGCAACAAAGTCCGCTCTGGGTGATGAGTCTGTCAATGCCAGCATTGACGGT
GCAGCATTCCGCGTGGGTGCAGGTGTACAAGCTGATATCACCAAAAACATGGGAGCATATGCAAGCCTTGACTACACCAA
AGGTGACGACATTGAGAACCCGCTACAGGGTGTAGTTGGTATCAATGTGACCTGG

Seq ID 153

ATGTCACGTCCGCAATTTACCTCGTTGCGTTTGAGTTTGTGGCTTTGGCTGTTTCTGCCACCTTGCCAACGTTTGCTTT
TGCTACTGAAACCATGACCGTTACGGCAACGGGAATGCACGTAGTTTCCTTCGAAGCGCCTATGATGGTCAGCGTTATCG
ACACTTCCGCTCCTGAAAATCAAACCTGCTACTTCAGCCACTGATTTGCTGCGTCATGTTCTTGGAACTTACTCTTGATGGT
ACCGGACGAACCAACGGTCAGGATGTAAATATGCGTGGCTATGATCATCGCGCGTGTGTTCTTGTGATGGTGTTCG
CCAGGGAACGGATACCGGACACCTGAATGGCACTTTTCTCGATCCGCGCGTGTATCAAGCGTGTGAGATTGTTCCGCGGAC
CTTCAGCATTACTGTATGGCAGTGGCGCGCTGGGTGGAGTGATCTCCTACGATACGGTCGATGCAAAAGATTTATTGCAG
GAAGGCAAAAGCAGTGGTTTTCGTGTCTTTGGTACTGGCGGCACGGGGGACCATAGCCTGGGATTAGGCGCGAGCGCGTT
TGGGCGAACTGAAAATCTGGATGGTATTGTGGCCTGGTCCAGTCGCGATCGGGGTGATTTACGCCAGAGCAATGGTGAAA
CCGCGCCGAATGACGAGTCCATTAATAACATGCTGGCGAAAGGGACCTGGCAAATTGATTACGCCAGTCTCTGAGCGGT
TTAGTGCCTTACTACAACAACGACGCGCGTGAACCAAAAAATCCGAGACCGTTGAAGCTTCTGATAGCAGCAACCCGAT
GGTCGATCGTTCAACAATTCAACGCGATGCGCAGCTTTCTTATAAACTCGCCCCGAGGGTAACGACTGGTTAAATGCAG
ATGCAAAAATTTACTGGTCGGAAGTCCGTATTAATGCGCAAAACACGGGGAGTTTACGGCGAGTATCGTGAAACAGATAACA
AAAGGAGCAAGGCTGGAGAACCGTTCCACTCTATTTGCCGACAGTTTCGCTTCTCACTTACTGACATATGGCGGTGAGTA
TTATCGTCAGGAACAACATCCGGGTGGCGCGACGACGGGCTTCCCGCAAGCAAAAATCGATTTTAGCTCTGGTTGGCTAC
AAGATGAGATCACCTTACGCGATCTGCCGATTACCTGCTTGGCGGAACCCGCTATGACAGTTATCGCGGTAGCAGCGAC
GGCTACAAAGATGTTGATGCCGACAAATGGTCATCTCGTGCGGGATGACTATCAACCCGACCAACTGGCTGATGTTATT
TGGCTCATATGCTCAGGCATTCGCGCGCCCCGACGATGGGCGAAATGTATAACGATTCTAAACACTTCTCGATTGGTTCGCT
TCTATACCAACTATTGGGTGCCAAAACCCGAACCTTACGTCGCGAAACTAACGAAACTCAGGAGTACGTTTGGGCTGCGT
TTTGATGACCTGATGTTGTCCAATGATGCTCTGGAATTTAAAGCCAGCTACTTTGATACCAAGCGAAAGATTATATCTC
CACGACCGTCGATTTCCGCGCGCGGACAACTATGTCTGTATAACGTCCCGAACGCCAAAATCTGGGGCTGGGATGTGATGA
CGAAATATACCACTGATCTGTTTAGCCTTGATGTGGCCTATAACCGTACCCGCGGCAAGACACCGATACCGGGGAATAT
ATCTCCAGCATTAAACCCGGATACCGTTACAGTACCTGAATATTCCGATCGCTCACAGCGGCTTCTCTGTTGGTTGGGT
CGGTACGTTTGGCGATCGCTCAACACATATCAGCAGCAGCTACAGCAAAACAACTGGCTATGGTGTGAATGATTTCTACG
TCAGTTATCAAGGGCAGCAGGCGCTCAAAGGCATGACCACTACTCTGGTATTGGGCAACGCCTTCGATAAAGAGTACTGG
TCGCGCAAGGCATCCACAGGATGGTCGTAACGGAAAAATTTTCGTGAGTTATCAATGG

Seq ID 154

ATGAGGGATGAAATGTTATATAATATACCTTGTGCAATTTATATCCTTTCCACTCTGTTCATTATGCATTTCTGGGATAGT
TTCTACTGCAACCGCAACTTCTTCAGAAACAAAATCAGCAACGAAGAGACGCTCGTCGTGACCACGAATCGTTCCGCAA
GCAACCTTTGGGAAAGCCCGGCGACTATACAGGTTATTGACCAACAAACATTGCAGAACTCCACCAATGCCTCCATAGCC
GATAATTTGCAGGACATCCCCGGAGTAGAGATAACAGACAACCTCCTTGGCAGGCCGTAACAAATCCGCATTTCGTGGCGA
AGCATCCTCCCGTGTGTTTAAATTTCTCATTTGATGGTCAGGAGGTAACCTTATCAGCGCGCCGGAGATAATTATGGTGTGGGAC
TGTTGATAGATGAGTCTGCGCTGGAGCGTGTGAGGTAGTGAAAGGTCCATATTCGGTACTGTACGGTTACAGGCAATT
GGCGGTATTGTTAACTTCATAACCAAAAAGGGAGGTGACAACTTGCATCTGGAGTTGTGAAAGCTGTTTATAATTCGCG
AACAGCAGGCTGGGAAGAATCAATCGCGGTCAGGGGAGCATCGGTGGATTGTGATTATCGCATCAACGGTAGTTATTTCTG
ATCAGGGCAATCGTGATACGCGGATGGACGCTCGGAATACCAACTATCGTAACAATAGTCAGGGTGTATGGTTGGGT
TATAACTCCGGAACCATCGTTTTGGCCTCTCGCTTGATCGCTACAGACTCGCGACGCAAACTTACTATGAGGATCCAGA
CGGAAGCTATGAGGCATTTAGTGTCAAAAATACCTAACTTGAACGAGAGAAAAGTTGGGGTATTCTATGACACAGACGTGG
ACGGTGACTATCTAAAAAAATTCATTTTCGACGCGTATGAGCAGACCATCCAGCGCCAATTTGCCAACGAAGTAAAAACG
ACACAGCCTGTTCCCGATCCGATGATTCAGGCTCTGACCGTTTATAACAAGACTGACACCCATGATAAGCAATACACTCA
GGCGGTACATTGCAGAGTCACTTTTCGCTGCCTGCTAATAATGAACCTGTTACCGGTGCACAGTACAAACAAGACAGGG
TCAGCCAAAGGTCCGGTGGCAGTACCTCAAGCAAATCTCTGACCGGCTTCATTAATAAGGAAACACGAACCTCGCTCCTAT
TATGAGTCAGAGCAAAGTACAGTCTCACTATTTCGCACAAAATGACTGGCGATTTCGCCGATCACTGGACATGGACAATGGG
AGTTCGCCAATACTGGCTTTCTTCAAAGTTGACGCGTGGTGACGGAGTATCATATACCGCAGGCATTATAAGCGATACCT
CTCTTGCCAGAGAGTCTGCGAGTGATCACGAAATGGTAACATCTACAAGCCTGCGCTATTACAGTTTCGATAACTTTGGAG
TTACGCGCTGCGTTTCGCGCAAGGCTACGTATTTCCACACTCTCCGACTTTTATGACAGACATCTCGGGCGGCGAGTGT
CACATACGGAATCCTGATCTTAAGGCTGAACACTCCAATAACTTTGAATTAGGTGCACGATATAATGGTAATACGTGGC
TGATTGACAGCGCAGTTTACTACTCAGAAGCTAAAGATTATATTGCAAGTCTGATCTGTGATGGCAGTATAGTTTGAAT
GGTAACACCAACTCCTCCCGTAGTAGTACTATTATTATGACAATATTGATCGGGCAAAAACATGGGGACTGGAAATAAG
CGCGGAATATAATGGCTGGGTTTTCTCGCCATATATCAGTGGCAATTTAATTCGTGCGCAATATGAAACTTCAACATTAA
AAACAATAATACAGGAGAACCAGCGATAAACGGACGTATAGGGCTGAAACATACTCTTGTGATGGGTGAGGCCAACATA
ATCTCTGATGTTTTTATTCGTGCTGCCTCTAGTGCAAAAGATGACAGTAACGGTACCGAAACAAATGTTCCGGGCTGGGC
CACTCTCAACTTTGCAGTAAATACAGAATTCGGTAACGAGGATCAGTCCCGGATTAACCTAGCACTCAATAACCTGACAG
ACAAACGCTACCGTACAGCACATGAAACTATTCTGCGAGCAGTTTTAATGCAGCTATAGGTTTTGTATGGAATTTT

Seq ID 155

ATGCGTAAAGTTTGTGCAGTCATTTTGTCCGCAGCCATCTGTCT
GTCCGTATCCGGTGC GCCTGCATGGGCGTCTGAACATCAGTCCACACTGAGCGCGGGGTA
TCTTCATGCCCCGTACGAACGCTCCCGGCAGCGATAATCTGAACGGGATTAACGTGAAATA
CCGTTATGAGTTTACGGACGCGCTGGGGCTGATTACGTCTTCAGTTATGCCAATGCTGA
GGATGAGCAAAAAACGCACTACAGCGATACCCGCTGGCATGAAGATTCCGTGCGTAACCG
CTGGTTCAGCGTGATGGCGGGGCGCTCTGTACGCGTGAATGAATGGTTCAGCGCGTATTC
GATGGCGGGTGTGGCTTACAGCCGTGTGTGCTGACTTTCTCCGGGGATTATCTCCGCGTAAC
TGACAACAAGGGGAAAAACGCACGATGTGCTGACCGGAAGTGATGACGGTCGCCACAGCAA
CACGTCTCTGGCGTGGGGGGCTGGCGTGCAGTTTAAACCCGACCGAATCCGTGACCATTGA
CCTTGCTTATGAAGTTCCGGTAGTGGCGACTGGCGAACGGATGCATTTATTGTTGGTAT
CGGATACCGTTTCTGA

Seq ID 156

ATGAAAAAATCGACATTATCTTTAGCCATCGGTTTATTATTGGCATGTAGTACCGGTATGGCAAAAACACAGCATTTAAC
GCTGGAACAACGCCTGGAAGCGGCAGAAATGCGGGCAGCAAAAGCAGAGGGGCAGGTTAAACAGCTTCAGACACAACAAG
CCGCCGAGATCCGCGAAATTAACACCGCACAGGGCAACACGCCGGTAAACGGTCAATCAACGACGGAGTCAGAGAAGAAA
AACGCCACCCCGCCTAATCTCTGCTTTTCAAGGTATGGCGATTTAAAAATCTACGGTGACGTAGAATTTAATATGGATGC
GGAAAGTAATCATGGCCTGTGGCAATGACCAACGCTGATGTGAATAGCGATCCCACTAATGAATGGAATCTCAATGGTC
GTATTCTGTTAGGTTTTGATGGTATGCGAAAACTGGATAATGGCTATTTTCGCTGGGTTCTCCGCACAACCGCTGGGGGAT
ATGCACGGTTCAGTAAATATCGATGATGCGGTTTTCTTCTTTGGCAAAGAAAAACGACTGGAAGGTCAAAGTAGGCCGTTT
TGAAGCCTACGATATGTTCCCGCTGAATCAGGATACCTTTGTTGAACATTCCGGTAATACTGCGAACGATCTTTATGACG
ATGGCAGCGGTTATATCTATATGATGAAAGAGGGCCGCGGACGTTCTAACGCTGGCGGTAATTTCTCGTCAGCAAAACAA
CTCGATAACTGGTATTTTGAATTAACACGTTACTGGAAGACGGAACATCTTTATATAACGACGGTAATTATCATGGACG
CGATATGGAACAGCAGAAAAATGTTGCTTATCTGCGTCCGGTAATTGCCTGGTCCGCCAGCGAAGAATTCACCGTTTCCG
CAGCGATGGAAGCGAATGTGGTAAATAATGCTTATGGTTATACCGATAGCAAGGGTAATTTTGTCTGATCAGTCCGATCGT
ACCGGTTATGGCATGAGTATGACCTGGAATGSCCTGAAAACCGATCCGGAAAAATGGCATCGTGGTTAATCTTAATACCGC
CTATTTAGATGCTAATAATGAAAAAGATTTACGGCAGGGATTAACGCGCTGTGGAAACGTTTCGAGCTGGGTTATATCT
ATGCACATAATAAGATTGATGAATTTAGTGGCGTGGTTTTGTTGATAACGATTGCTGGATTGATGATGAAGGAACATAACAAC
ATTCACACCATTCATGCGTCTTATCAGTTTCGCTAATGTGATGGATATGGAGAACCTTTAATATTTACCTCGGCACGTATTA
CTCCATTCTGGATAGCGACGGCGATAAGATACACGGCGACGATAGTGATGACCGTTACGGCGCACGCGTTTCGCTTTAAAT
ACTTCTTC

Seq ID 157

ATGAACGGCAAAAGCGTTTCTGGCCTGCGTTCTGATGAGCGTCGTATTAACTGGCTGTGAAACAGCGAAAAAATCAGCCA
GGTGATCCGCAATCCGGATATTTCAGGTTCGGAAGCTGATGGATCAGTCAACCGAGCTGACCGTCACGCTGCTGACCGAGC
CGGACAGCAACCTGACGGCGGATGGCGAAGCCGCGCGGTGGATGTCCAGTTGGTTTATCTGAGCGACGACTCAAAATTC
CATGCCCGGACTACGACAGGTTGCCACCACCGCGCTGCCCGACGTGCTGGGGAAAAAATATATCGATCACCAGGACTT
CAACCTGTTGCCGATACCGTTAAAAACACTGCCCGCGATCAAGTTGGATGAGAAAACCGGTTATATCGGTGTCTATTGCCT
ATTTTTTCAGACGACGAGCCACAGAAATGGAACAAATTGATCGGTAGAAAGTATCGGCCACCACCTATCGCCTGCTGGTG
CATATCCGCGCCAGTGCGATTGAGATGAAAAAAGAGAAAAAC

Seq ID 158

CTGACGCTGGCATGGATTTTTCTGCTGGTGTGGATCTGGTGGCAGGGTCCAAAATGGACGCTCTATGAGCAGCACTGGCT
GGCTCCGCTGGCAAACCGCTGGCTGGCGACCGCCGTCTGGGGACTTATCGCTCTGGTCTGGCTCACCTGGCGGGTGATGA
AGCGTCTGCAAAAGCTGGAAAAACAGCAGAAACAGCAGCGGGAGGAAGAAAAAGATCCGTTGACCGTGGAATCCACCGC
CAGCAGCAATATCTGGATCACTGGCTGCTGCGCCTGCGCCGCCATCTGGATAACCGCCGTTATCTGTGGCAGTTGCCGTG
GTATATGGTCATTGGTCTGCGGGTAGCGGCAAAAGCACGCTGCTGCGCGAGGGCTTTCCGCTGACATTGTTTACACGC
CGGAAAGCATCCGGGGGTGGAATACCACCCGCTGATCACACCGCGAGTGGGCAACCAGGCGGTAATTTTCGATGTTGAC
GGCGTACTGACCACTCCCGGCGGGATGATCTGCTCCGCCCGCCCTGCGCGAACACTGGCTGGGCTGGCTGATGCAAAC
GCGCGCTCGCCAGCCGCTCAACGGTCTTATCTGACGCTCGATCTTCCGATCTGCTGACGGCGGATAAATCCCGCCGTG
AGACACTGGTACAAAATTTGCGCCAGCAACTTCAGGAGATCCGTACAGCTGCCTGACTGCCGCTGCCCCGTTTACGTGGTG
CTGACACGGCTGGATCTGCTGAACGGCTTTGCGCGCTGTTCCATTCACTGGATAAAAAAGACCGCGATGCGATCCTCGG
CGTCACATTTACCCGCCGCGCCCATGAAAGTGACGGCTGGCGCAGCGAATGGGGGCTTTCTGGCAGACGTGGGTACAAC
AGGTGAACCTGGCGCTGTGCGATCTGGTGCTCGCACAAACCGGTGCTGCTCCCCGACGCGCTGTGTTTACGTTCTCCCGT
CAGATGCAGGGAACAGGAGAAATCGTCAACCGCACTGCTCGCCGATTTGCTGGACGGTGAGAACATGGATGTAATGCTGCG
TGGCGTCTGGCTCACATCCTCGCTACAGCGTGGCCAGGTGGATGATATTTTACGCAGTCCGCCGCCCGCCAGTACGGAC

TGGGTAACAGCTCGCTGGCAACCTGGCCTCTGGTGGAGACGACGCCGTATTTTACTCGCCGCCTCTTCCCGGAAGTCCTG
CTGGCTGAGCCGAACCTGGCGGGTGAAAACAGCGTCTGGCTGAACAGCTCCCGGCGCAGGCTGACCGCCTTTTCCACCTG
TGGCGCGGCACTGGCGGCATTGATGGTCGGAAGCTGGCACCATTATTACAATCAGAACTGGCAGTCTGGCGTTAACGTAC
TGGCACAAGCTAAAGCCTTTATGGACGTACCACCACCGCAGGGAACGGATGAATTCGGCAATCTGCAATTGCCATTGCTT
AACCCGGTACGCGATGCCACCCTGGCCTATGGTGATTATCGCGATCACGGTTTTCTGGCGGATATGGGATTGTACCAGGG
CGCCCGCTAGGGCCGTATGTGGAGCAAACCTACATTTCAGCTTCTTTGAGCAGCGTTATCTCCCTCGTTAATGAACGGCC
TGATCCGGGATCTAAACATTGCCCCGCCAGAGAGCGAAGAAAAGCTCGCTGTGCTGCGCGTAGTGCGCATGATGGAAGAC
AAAAGTGGGCGCAACAACGAGGCGGTAAAACAGTACATGGCACGGCGCTGGAGCAATGAATTTACGGCCAGCGCGATAT
TCAGGCGCAACTGATGGTGATCTGGACTATGCGCTGGAGCACACCGACTGGCACGCGCAGCGCCAAAGCAGCGACAGCG
ATGCTGTTCAGCCGCTGGACCCCTATGATAAACCGATCATTAAATGCGCAGCAGGAACTGAGCAAGCTGCCCATATACCAG
CGTGTCTACCAGACCCTGCGCACCAAGCATTAAAGCGTGTGTCGCCGCGGATTGTAATTTGCGCGACCAGGTTGGTCCCAC
CTTCGACAACGTGTTCTGTCGCCGGTAATGATGAAAACTGGTGATCCCGCAGTTTCTCACCCGCTATGGACTGCAAAGCT
ATTTTGTCAAACAGCGTGAGGGCCTCGTTGAGCTGACCGCGCTGGATTCTGTGGGTACTGAACCTGACGCAAAGCGTCGCC
TACAGCGAGGCGGACCGTGAAGAGATCCAGCGCCATATCACCGAACAGTACATCAGTGACTATACCGCCACCTGGCGTGC
CGGAATGGATAACCTCAACGTCCGTGACTATGAGGCCATGTCGGCGCTGACCGACGCGCTGGAGCAGATTATCAGCGGCG
ATCAGCCATTCCAGCGTGCGCTGACGGCGCTGCGCGATAATACCCACGCGCTGACGCTCTCCGGCAAACCTGGATGATAAG
GCGAGGGAAGCGGCGATAAATGAGATGGATTACCGCCTGTTATCCCGGCTGGGGCATGAGTTTCGCACCGGAAAACAGCGC
ACTGGAGGAGCAAAAGGACAAGGCGAGTACGCTACAGGCCGTGTACCAGCAACTGACCGAGCTGCACCGTTACCTGCTGG
CGATCCAGAACTCGCCAGTGCCGGGGAAATCGGCGCTGAAAGCAGTACAGCTACGGCTGGATCAAAAACAGCAGCGATCCA
ATCTTCGCCACCCGTGATGGTGAAGCCGTTTCGTTACATGGAAGTGGACTGGCGCGACAATGTAGTGAAACCCCTTCAACGAGCAGC
TTGCCGATAACTATCCGTTTAAATCCGCGCGCCACACAGGATGCCTCACTGGATTCTGTTTGAACGTTTCTTTAAACCGGAT
GGCATTCTGGACAATTTCTACAAGAACAACCTGCGCCTGTTTCTTGAACGATCTGACCTTTGGCGACGACGGCAGAGT
GTTAATCCGTGAAGATATCCGGCAGCAACTGGATAACCGCGCAGAAAAATCCGCGACATCTTCTTACGCCAGCAGAACGGGC
TGGGCGCACAGTTTCCCGTGGAAACCGTATCGCTTTCCGGCAATAAGCGGCGCAGCGTACTTAACCTGGACGGCCAGTTA
GTGGACTACAGCCAGGACGCAACTACACCGCCCATCTGGTCTGGCCGAACAACATGCGTGAAGGCAATGAAAGCAAGCT
GACGCTGATTGGCACCAGCGGCGAGACACCGCGCAGTATCGCGTTCAGTGGACCGTGGGCGCAGTTCCGCCTGTTCCGGCG
CGGGCCAGTTGACCAATGTGACCAGTGACACCTTTAACGTGCGCTTTAACGTGGACGGCGGCGCAATGGTTTACCAGGTG
CATGTGGATACCGAAGATAACCCGTTTACCGGCGGTCTGTTTACGCTGTTCCGTTTACCGGATACGTTGTAT

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
12 September 2003 (12.09.2003)

PCT

(10) International Publication Number
WO 2003/074553 A3

(51) International Patent Classification⁷: **C12N 15/31**,
15/63, C07K 14/245, 16/12, A61K 39/108, G01N 33/53

(21) International Application Number:
PCT/EP2003/002925

(22) International Filing Date: 6 March 2003 (06.03.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
02290556.6 6 March 2002 (06.03.2002) EP

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): MUTA-BILIS SA [FR/FR]; 13, rue de Toul, F-75012 Paris (FR).

(72) Inventor; and

(75) Inventor/Applicant (*for US only*): ESCAICH, Sonia [FR/FR]; 13, rue de Toul, F-75012 Paris (FR).

(74) Agents: PEAUCELLE, Chantal et al.; Cabinet Armen-gaud Aine, 3, Avenue Bugeaud, F-75116 Paris (FR).

Published:

— with international search report

(88) Date of publication of the international search report:
25 March 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: EXPEC-SPECIFIC PROTEINS, GENES ENCODING THEM AND USES THEREOF

(57) Abstract: The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of: 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria, 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates, 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates, 4- testing the polypeptides for immunogenicity using animals models. Application for making vaccines compositions and immunotherapies

WO 2003/074553 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 03/02925

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/63 C07K14/245 C07K16/12 A61K39/108
G01N33/53

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 66572 A (INST NAT SANTE RECH MED ;NASSIF XAVIER (FR); TINSLEY COLIN (FR); B) 13 September 2001 (2001-09-13) SEQ ID NOs:390 and 391 page 3, line 20 - page 4, line 17 page 29, line 23 - line 31 -----	1-6, 9-13,15, 16
A	JOHNSON JAMES R ET AL: "Phylogenetic and pathotypic similarities between Escherichia coli isolates from urinary tract infections in dogs and extraintestinal infections in humans." JOURNAL OF INFECTIOUS DISEASES, vol. 183, no. 6, 2001, pages 897-906, XP002211433 ISSN: 0022-1899 abstract ----- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

11 August 2003

Date of mailing of the international search report

05.12.2003

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Mata-Vicente, M.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 03/02925

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>MUEHLDOERFER I ET AL: "Characterization of Escherichia coli strains isolated from environmental water habitats and from stool samples of healthy volunteers." RESEARCH IN MICROBIOLOGY, vol. 147, no. 8, 1996, pages 625-635, XP002211434 ISSN: 0923-2508 table I page 630, paragraph 2 -----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 03/02925

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet) -

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.: 14
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-6, 9-13, 15 and 16 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

As far as an "in vivo" method is concerned, claim 9 is directed to a method of treatment of the human/animal body and the search has been carried out and based on the alleged effects of the compound/composition.

As far as an "in vivo" method is concerned, claim 15 is directed to a diagnostic method practised on the human/animal body and the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.2

Claims Nos.: 14

Claim 14 refers to "monoclonal antibodies against epitopes of polypeptide", but it does not say which polypeptide is meant. In consequence, the scope of said claim is ambiguous and vague and its subject-matter is not sufficiently disclosed and supported (Art. 83 and 84 EPC). Therefore, no search has been carried out on said claim.

The phrase "polypeptide such as used according to claim 9" comprised in Claim 13 lacks any sense. Nevertheless, the ISA has assumed that it is an error and that it refers to the polypeptides referred to in Claim 9 or, in other words, a polypeptide selected from the group comprising SEQ ID NOs:1-66 (except SEQ ID NO:8) and 133-145.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims (1-6, 9-13, 15 and 16) - partially

Isolated antigenic polypeptide SEQ ID NO:14; the polynucleotide encoding it (SEQ ID NO:80); vector comprising said polynucleotide and host cell transformed with it; antibodies against said polypeptide; vaccines comprising the polypeptide; methods of diagnosis/treatment derived of the use of any of the molecules previously mentioned.

Inventions 2-32: Claims (1-6, 9-13, 15 and 16) - partially

Idem as invention 1, but restricted to each one of the polypeptides of SEQ ID NOs: 15, 17, 21-23, 28-30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52-55, 58, 60, 63 and 133-138 and their corresponding genes (SEQ ID NOs:81, 83, 87-89, 94-96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119 and 126).

Invention 33: Claims (4-6) - partially

Isolated polynucleotide SEQ ID NO:127, vector comprising it and host cell transformed therewith.

Inventions 34-41: Claims (9-13, 15 and 16) - partially

Idem as invention 33, but restricted to each one of the polynucleotides SEQ ID NOs: 130, 132 and 146-151.

Invention 42: Claims (9-13, 15 and 16) - partially

Use of the polypeptide SEQ ID NO:1 as antigen; vaccines; antibodies against said polypeptide; methods of diagnosis/treatment derived of the use thereof.

Inventions 43-86: Claims (9-13, 15 and 16) - partially

Idem as invention 42, but restricted to each one of the polypeptides SEQ ID NOs: 2-7, 9-13, 16, 18-20, 24-27, 31, 33-35, 37, 40, 45, 47, 48, 51, 56, 57, 59, 61, 62, 64-66, 139-145.

Invention 87: Claims (7 and 8) - completely.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Process for isolating and identifying polypeptides useful as vaccines comprising the steps of: selecting on the basis of sequence analysis those of the polypeptides which are either located in the outer membrane or secreted by the bacteria; identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates; purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates; and testing the polypeptides for immunogenicity using animal models.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 03/02925

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 0166572	A	13-09-2001	FR 2806096 A1	14-09-2001
			CA 2402602 A1	13-09-2001
			WO 0166572 A2	13-09-2001
			EP 1328641 A2	23-07-2003
			US 2003148324 A1	07-08-2003

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.